OM nucleic - nucleic search, using sw model

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 04:08:08 ; Search time 1358.3 Seconds
(without alignments)
16712.222 Million cell updates/sec

Title: US-09-869-894-1
Perfect score: 780
Sequence: 1 gagtgagcattctcagcaca.........aattgtatgtattttctct 780

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size :   0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_pr:*
27: em_ro:*
28: em_sts:*
29: em_un:*
30: em_vi:*
31: em_htg_hum:*
32: em_htg_inv:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1	C	28	3.6	28	6	AR091102	AR091102 Sequence
2	C	28	3.6	28	6	AR198137	AR198137 Sequence
3	C	26	3.3	26	6	AR091101	AR091101 Sequence
4	C	26	3.3	26	6	AR198136	AR198136 Sequence
5	C	22	2.6	22	6	AR095064	AR095064 Sequence
6	C	20	2.6	20	6	AR095049	AR095049 Sequence
7	C	20	2.6	20	6	AR095050	AR095050 Sequence
8	C	20	2.6	20	6	AR095051	AR095051 Sequence
9	C	20	2.6	20	6	AR095052	AR095052 Sequence
10	C	20	2.6	20	6	AR095053	AR095053 Sequence
11	C	20	2.6	20	6	AR095054	AR095054 Sequence
12	C	20	2.6	20	6	AR095055	AR095055 Sequence
13	C	20	2.6	20	6	AR095056	AR095056 Sequence
14	C	20	2.6	20	6	AR095057	AR095057 Sequence
15	C	20	2.6	20	6	AR095058	AR095058 Sequence
16	C	20	2.6	20	6	AR095059	AR095059 Sequence
17	C	20	2.6	20	6	AR095060	AR095060 Sequence
18	C	20	2.6	20	6	AR095061	AR095061 Sequence
19	C	20	2.6	20	6	AR095062	AR095062 Sequence
20	C	20	2.6	20	6	AR095063	AR095063 Sequence
21	C	16	2.6	20	6	A22329	A22329 Primer O-3
22	C	16	2.1	43	6	A22330	A22330 Primer O-3
23	C	15	1.9	32	6	AX236036	AX236036 Sequence
24	C	14	1.8	19	6	AX132760	AX132760 Sequence
25	C	14	1.8	19	6	AX132761	AX132761 Sequence
26	C	14	1.8	19	6	AX132762	AX132762 Sequence
27	C	14	1.8	19	6	AX132763	AX132763 Sequence
28	C	14	1.8	19	6	AX132764	AX132764 Sequence
29	C	14	1.8	20	6	AX008457	AX008457 Sequence
30	C	14	1.8	20	6	AX020687	AX020687 Sequence
31	C	14	1.8	20	6	AX045382	AX045382 Sequence
32	C	14	1.8	20	6	AX045383	AX045383 Sequence
33	C	14	1.8	20	6	AX045385	AX045385 Sequence
34	C	14	1.8	20	6	AX482149	AX482149 Sequence
35	C	14	1.8	27	6	AX069502	AX069502 Sequence
36	C	14	1.8	27	6	AR040695	AR040695 Sequence
37	C	14	1.8	27	6	AR195122	AR195122 Sequence
38	C	14	1.8	27	6	AX203850	AX203850 Sequence
39	C	14	1.8	27	6	AX469912	AX469912 Sequence
40	C	14	1.8	30	6	AR070762	AR070762 Sequence
41	C	14	1.8	30	6	AR122968	AR122968 Sequence
42	C	14	1.8	30	6	BD005404	BD005404 Protein i
43	C	14	1.8	31	6	AX059211	AX059211 Sequence
44	C	14	1.8	31	6	I28164	I28164 Sequence 7
45	C	14	1.8	35	6	AX474377	AX474377 Sequence

ALIGNMENTS

RESULT 1
AR091102/c

LOCUS   AR091102   28 bp   DNA   linear   PAT 07-SEP-2000
DEFINITION Sequence 1222 from patent US 5994076.
ACCESSION   AR091102
VERSION   AR091102.1 GI:10017857
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE   Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 1222 30-NOV-1999;
FEATURES   Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

```
                source          1..28
BASE COUNT       6 a     4 c      9 g     9 t
ORIGIN
        /organism="unknown"

Qy  265 TCCGTAGACACTGCCAGAACACTATTCA 292
        ||||||||||||||||||||||||||||
Db   28 TCCGTAGACACTGCCAGAACACTATTCA 1

RESULT 2
AR198137/c
LOCUS       AR198137              28 bp    DNA      linear   PAT 20-APR-2002
DEFINITION  Sequence 1222 from patent US 6352829.
ACCESSION   AR198137
VERSION     AR198137.1  GI:20247986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 1222 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..28
                     /organism="unknown"

Query Match             100.0%;  Score 28;  DB 6;  Length 28;
Best Local Similarity   3.6%;    Pred. No. 0.0038;
Matches    28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy  265 TCCGTAGACACTGCCAGAACACTATTCA 292
        ||||||||||||||||||||||||||||
Db   28 TCCGTAGACACTGCCAGAACACTATTCA 1

RESULT 3
AR091101
LOCUS       AR091101              26 bp    DNA      linear   PAT 07-SEP-2000
DEFINITION  Sequence 1221 from patent US 5994076.
ACCESSION   AR091101
VERSION     AR091101.1  GI:10017856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 1221 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1..26
                     /organism="unknown"
BASE COUNT       9 a     7 c      7 g     3 t
ORIGIN

Query Match             100.0%;  Score 26;  DB 6;  Length 26;
Best Local Similarity   3.3%;    Pred. No. 0.046;
Matches    26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   64 TCCACCAGGCCAGAAGAGATGACAGACTG 89
        ||||||||||||||||||||||||||
Db    1 TCCACCAGGCCAGAAGAGATGACAGACTG 26

RESULT 4
```

```
AR198136
LOCUS       AR198136             26 bp     DNA      linear   PAT 20-APR-2002
DEFINITION  Sequence 1221 from patent US 6352829.
ACCESSION   AR198136
VERSION     AR198136.1  GI:20247985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 1221 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..26
                     /organism="unknown"
BASE COUNT       9 a     7 c      7 g     3 t
ORIGIN

Query Match             100.0%;  Score 26;  DB 6;  Length 26;
Best Local Similarity   3.3%;    Pred. No. 0.046;
Matches    26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   64 TCCACCAGGCCAGAAGAGATGACAGACTG 89
        ||||||||||||||||||||||||||
Db    1 TCCACCAGGCCAGAAGAGATGACAGACTG 26

RESULT 5
AR095064/c
LOCUS       AR095064              22 bp    DNA      linear   PAT 08-SEP-2000
DEFINITION  Sequence 17 from patent US 6001992.
ACCESSION   AR095064
VERSION     AR095064.1  GI:10022579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 17 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..22
                     /organism="unknown"
BASE COUNT       6 a     2 c      7 g     7 t
ORIGIN

Query Match             100.0%;  Score 22;  DB 6;  Length 22;
Best Local Similarity   2.8%;    Pred. No. 6.8;
Matches    22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy  663 ACGATTGCCAACACATACTTCT 684
        ||||||||||||||||||||||
Db   22 ACGATTGCCAACACATACTTCT 1

RESULT 6
AR095049/c
LOCUS       AR095049              20 bp    DNA      linear   PAT 08-SEP-2000
DEFINITION  Sequence 2 from patent US 6001992.
ACCESSION   AR095049
VERSION     AR095049.1  GI:10022549
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 2 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
```

BASE COUNT   4 a   5 c   5 g   6 t
ORIGIN
     source   1..20
                     /organism="unknown"

Best Local Similarity 100.0%;
Query Match   2.6%;   Score 20;   DB 6;   Length 20;
Matches   20;   Conservative   0;   Mismatches   0;   Pred. No. 83;   Indels   0;   Gaps   0;

Qy   1 GACTGACCATTCTCAGCACA 20
        ||||||||||||||||||||
Db   20 GAGTGAGCATTCTCAGCACA 1

RESULT 7
LOCUS   AR095050/c   20 bp   DNA   linear   PAT 08-SEP-2000
DEFINITION Sequence 3 from patent US 6001992.
ACCESSION   AR095050
VERSION   AR095050.1   GI:10022551
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 3 14-DEC-1999;
FEATURES   Location/Qualifiers
     source   1..20
                     /organism="unknown"
BASE COUNT   5 a   2 c   7 g   6 t
ORIGIN

Best Local Similarity 100.0%;
Query Match   2.6%;   Score 20;   DB 6;   Length 20;
Matches   20;   Conservative   0;   Mismatches   0;   Pred. No. 83;   Indels   0;   Gaps   0;

Qy   19 CAATGCCTCAACAGCTTCAA 38
        ||||||||||||||||||||
Db   20 CAATGCCTCAACAGCTTCAA 1

RESULT 8
LOCUS   AR095051/c   20 bp   DNA   linear   PAT 08-SEP-2000
DEFINITION Sequence 4 from patent US 6001992.
ACCESSION   AR095051
VERSION   AR095051.1   GI:10022553
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 4 14-DEC-1999;
FEATURES   Location/Qualifiers
     source   1..20
                     /organism="unknown"
BASE COUNT   4 a   6 c   5 g   5 t
ORIGIN

Best Local Similarity 100.0%;
Query Match   2.6%;   Score 20;   DB 6;   Length 20;
Matches   20;   Conservative   0;   Mismatches   0;   Pred. No. 83;   Indels   0;   Gaps   0;

Qy   39 GGTGAGCCAGCTCAAGACTT 58
        ||||||||||||||||||||
Db   20 GGTGAGCCAGCTCAAGACTT 1

RESULT 9
LOCUS   AR095052/c   20 bp   DNA   linear   PAT 08-SEP-2000
DEFINITION Sequence 5 from patent US 6001992.
ACCESSION   AR095052
VERSION   AR095052.1   GI:10022555
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 5 14-DEC-1999;
FEATURES   Location/Qualifiers
     source   1..20
                     /organism="unknown"
BASE COUNT   6 a   4 c   5 g   5 t
ORIGIN

Best Local Similarity 100.0%;
Query Match   2.6%;   Score 20;   DB 6;   Length 20;
Matches   20;   Conservative   0;   Mismatches   0;   Pred. No. 83;   Indels   0;   Gaps   0;

Qy   66 CACCAGGCAGAAGATGACAG 85
        ||||||||||||||||||||
Db   20 CACCAGGCAGAAGATGACAG 1

RESULT 10
LOCUS   AR095053/c   20 bp   DNA   linear   PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 6001992.
ACCESSION   AR095053
VERSION   AR095053.1   GI:10022557
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 6 14-DEC-1999;
FEATURES   Location/Qualifiers
     source   1..20
                     /organism="unknown"
BASE COUNT   8 a   4 c   1 g   7 t
ORIGIN

Best Local Similarity 100.0%;
Query Match   2.6%;   Score 20;   DB 6;   Length 20;
Matches   20;   Conservative   0;   Mismatches   0;   Pred. No. 83;   Indels   0;   Gaps   0;

Qy   91 GAATTTGGATATATTTACAG 110
        ||||||||||||||||||||
Db   20 GAATTTGGATATATTTACAG 1

RESULT 11
LOCUS   AR095054/c   20 bp   DNA   linear   PAT 08-SEP-2000
DEFINITION Sequence 7 from patent US 6001992.
ACCESSION   AR095054
VERSION   AR095054.1   GI:10022559
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 7 14-DEC-1999;
FEATURES   Location/Qualifiers
     source   1..20
                     /organism="unknown"

BASE COUNT   5 a   6 c   6 g   3 t
ORIGIN

Qy   111 GCTGGCTCAGGACTATCTGC 130
              ||||||||||||||||||||
Db   20 GCTGGCTCAGGACTATCTGC 1

RESULT 12
LOCUS   AR095055   20 bp   DNA   linear   PAT 08-SEP-2000
AR095055/c
DEFINITION   Sequence 8 from patent US 6001992.
ACCESSION   AR095055
VERSION   AR095055.1 GI:10022561
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS   Ackerman,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL   Patent: US 6001992-A 8 14-DEC-1999;
FEATURES   Location/Qualifiers
  source   1..20
                     /organism="unknown"

BASE COUNT   7 a   4 c   5 g   4 t
ORIGIN

Query Match   2.68%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   193 AATGTTGCGTTCTCAGTCCA 212
              ||||||||||||||||||||
Db   20 AATGTTGCGTTCTCAGTCCA 1

RESULT 13
LOCUS   AR095056   20 bp   DNA   linear   PAT 08-SEP-2000
AR095056/c
DEFINITION   Sequence 9 from patent US 6001992.
ACCESSION   AR095056
VERSION   AR095056.1 GI:10022563
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS   Ackerman,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL   Patent: US 6001992-A 9 14-DEC-1999;
FEATURES   Location/Qualifiers
  source   1..20
                     /organism="unknown"

BASE COUNT   4 a   3 c   6 g   7 t
ORIGIN

Query Match   2.68%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   271 GACACTGCCAGAGACACTATT 290
              ||||||||||||||||||||
Db   20 GACACTGCCAGAGACACTATT 1

RESULT 14
LOCUS   AR095057   20 bp   DNA   linear   PAT 08-SEP-2000
AR095057/c

DEFINITION   Sequence 10 from patent US 6001992.
ACCESSION   AR095057
VERSION   AR095057.1 GI:10022565
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL   Patent: US 6001992-A 10 14-DEC-1999;
FEATURES   Location/Qualifiers
  source   1..20
                     /organism="unknown"

BASE COUNT   4 a   7 c   3 g   6 t
ORIGIN

Query Match   2.68%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   309 GGAGTTTGAAGACGGCATCA 328
              ||||||||||||||||||||
Db   20 GGAGTTTGAAGACGGCATCA 1

RESULT 15
LOCUS   AR095058   20 bp   DNA   linear   PAT 08-SEP-2000
AR095058/c
DEFINITION   Sequence 11 from patent US 6001992.
ACCESSION   AR095058
VERSION   AR095058.1 GI:10022567
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE   Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL   Patent: US 6001992-A 11 14-DEC-1999;
FEATURES   Location/Qualifiers
  source   1..20
                     /organism="unknown"

BASE COUNT   3 a   3 c   5 g   9 t
ORIGIN

Query Match   2.68%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   379 AAGAAACTTCTACGACAGCA 398
              ||||||||||||||||||||
Db   20 AAGAAACTTCTACGACAGCA 1

Search completed: March 14, 2003, 07:13:17
Job time : 1363.8 secs

```
OM nucleic - nucleic search, using sw model

                        GenCore version 5.1.4_p5_4578
                        Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:                 March 14, 2003, 04:33:38 ; Search time 18.863 Seconds
                                                   (without alignments)
                                                   12681.353 Million cell updates/sec

Title:                  780
Perfect score:          780
Sequence:               1 gagtgagcattctcagacaca...........aattgtatgtattttctct 780

Scoring table:          OLIGO_NUC
                        Gapop 60.0 , Gapext 60.0

Searched:               441362 seqs, 153338381 residues

Word size :             0

Total number of hits satisfying chosen parameters:        609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :              Issued_Patents_NA:*
                        1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                        2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                        3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                        4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                        5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                        6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	3.6	28	2	US-08-859-998-1222	Sequence 1222, Ap
2	28	3.6	28	4	US-09-225-928-1222	Sequence 1222, Ap
3	26	3.3	26	4	US-08-859-998-1221	Sequence 1221, Ap
c 4	26	3.3	26	4	US-08-533-472-3	Sequence 3, Appl
5	22	2.8	22	3	US-09-225-928-1221	Sequence 1221, Ap
c 6	22	2.8	22	3	US-09-226-568-17	Sequence 17, Appl
7	20	2.6	20	3	US-09-226-568-2	Sequence 2, Appl
c 8	20	2.6	20	3	US-09-226-568-3	Sequence 3, Appl
c 9	20	2.6	20	3	US-09-226-568-4	Sequence 4, Appl
c 10	20	2.6	20	3	US-09-226-568-5	Sequence 5, Appl
c 11	20	2.6	20	3	US-09-226-568-6	Sequence 6, Appl
c 12	20	2.6	20	3	US-09-226-568-7	Sequence 7, Appl
c 13	20	2.6	20	3	US-09-226-568-9	Sequence 9, Appl
c 14	20	2.6	20	3	US-09-226-568-10	Sequence 10, Appl
c 15	20	2.6	20	3	US-09-226-568-11	Sequence 11, Appl
c 16	20	2.6	20	3	US-09-226-568-12	Sequence 12, Appl
c 17	20	2.6	20	3	US-09-226-568-13	Sequence 13, Appl
c 18	20	2.6	20	3	US-09-226-568-14	Sequence 14, Appl
c 19	20	2.6	20	3	US-09-226-568-15	Sequence 15, Appl
c 20	20	2.6	20	3	US-09-226-568-16	Sequence 16, Appl
c 21	20	2.6	20	1	US-09-226-568-17	Sequence 17, Appl
c 22	14	1.8	27	2	US-08-977-818-17	Sequence 17, Appl
c 23	14	1.8	27	2	US-08-670-274B-17	Sequence 17, Appl
c 24	14	1.8	27	4	US-09-146-187-17	Sequence 17, Appl
c 25	14	1.8	27	4	US-09-514-599-8	Sequence 8, Appl
c 26	14	1.8	30	4	US-08-705-625-10	Sequence 10, Appl
27	14	1.8	30	4	US-09-220-574-10	Sequence 10, Appl
28	14	1.8	31	1	US-09-328-750A-4	Sequence 4, Appl
29	14	1.8	31	5	PCT-US94-05821A-7	Sequence 7, Appl
30	13	1.7	14	1	US-08-598-591-71	Sequence 71, Appl
31	13	1.7	14	1	US-08-533-472-3	Sequence 3, Appl
32	13	1.7	14	3	US-08-988-706-48	Sequence 48, Appl
33	13	1.7	19	2	US-08-117-952-254	Sequence 254, App
c 34	13	1.7	20	1	US-08-598-591-56	Sequence 56, Appl
c 35	13	1.7	20	1	US-08-798-691-60	Sequence 60, Appl
c 36	13	1.7	20	1	US-09-607-384A-30	Sequence 30, Appl
c 37	13	1.7	20	2	US-09-038-227-21	Sequence 21, Appl
c 38	13	1.7	20	3	US-08-825-487A-60	Sequence 60, Appl
c 39	13	1.7	20	3	US-08-988-706-31	Sequence 31, Appl
c 40	13	1.7	20	4	US-09-074-476-60	Sequence 60, Appl
c 41	13	1.7	21	4	US-08-988-706-21	Sequence 21, Appl
c 42	13	1.7	21	4	US-08-928-941D-34	Sequence 34, Appl
c 43	13	1.7	21	4	US-09-280-590A-44	Sequence 44, Appl
44	13	1.7	22	1	US-08-105-761-9	Sequence 9, Appl
45	13	1.7	22	1	US-08-060-925A-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-08-859-998-1222/c
; Sequence 1222, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT: Jokhadze, George
;  APPLICANT: Bibilashvili, Robert
;  TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;  TITLE OF INVENTION: EXPRESSION
;  NUMBER OF SEQUENCES: 1375
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 2200 Sand Hill Road, Suite 100
;   CITY: Menlo Park
;   STATE: CA
;   COUNTRY: US
;   ZIP: 94025
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/859,998
;   FILING DATE: 21-MAY-1997
;   CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Field, Bret E.
;   REGISTRATION NUMBER: 37,620
;   REFERENCE/DOCKET NUMBER: 09096/002001
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-322-5070
;   TELEFAX: 415-854-0875
;  INFORMATION FOR SEQ ID NO: 1222:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 28 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;    OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1222

  Query Match                 3.6%;  Score 28;  DB 2;  Length 28;
  Best Local Similarity     100.0%;  Pred. No. 7.2e-05;
```

```
Qy   265 TCCGTAGACACTGCCAGAACACTATTCA 292
         ||||||||||||||||||||||||||||
Db    28 TCCGTAGACACTGCCAGAACACTATTCA 1
```

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-225-928-1222/c
Sequence 1222, Application US/09225928
Patent No. 6352829
  GENERAL INFORMATION:
     APPLICANT: Chenchik, Alex
              Jokhadze, George
              Bibilashvilli, Robert
     TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
              EXPRESSION
     NUMBER OF SEQUENCES: 1375
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: Fish & Richardson, P.C.
        STREET: 2200 Sand Hill Road, Suite 100
        CITY: Menlo Park
        STATE: CA
        COUNTRY: US
        ZIP: 94025
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: Windows95
        SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/225,928
        FILING DATE: 05-Jan-1999
        CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/859,998
        FILING DATE: 21-MAY-1997
     ATTORNEY/AGENT INFORMATION:
        NAME: Field, Bret E.
        REGISTRATION NUMBER: 37,620
        REFERENCE/DOCKET NUMBER: 09096/002001
     TELECOMMUNICATION INFORMATION:
        TELEPHONE: 415-322-5070
        TELEFAX: 415-854-0875
     INFORMATION FOR SEQ ID NO: 1222:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 28 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
     MOLECULE TYPE: DNA
     FEATURE:
        OTHER INFORMATION: oligonucleotide primer
     SEQUENCE DESCRIPTION: SEQ ID NO: 1222:
US-08-859-998-1221

```
Qy   265 TCCGTAGACACTGCCAGAACACTATTCA 292
         ||||||||||||||||||||||||||||
Db    28 TCCGTAGACACTGCCAGAACACTATTCA 1
```

Query Match   3.68; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-08-859-998-1221
Sequence 1221, Application US/08859998
Patent No. 5994076
  GENERAL INFORMATION:
     APPLICANT: Chenchik, Alex
     APPLICANT: Jokhadze, George
     APPLICANT: Bibilashvilli, Robert

     TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
     TITLE OF INVENTION: EXPRESSION
     NUMBER OF SEQUENCES: 1375
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: Fish & Richardson, P.C.
        STREET: 2200 Sand Hill Road, Suite 100
        CITY: Menlo Park
        STATE: CA
        COUNTRY: US
        ZIP: 94025
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: Windows95
        SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/859,998
        FILING DATE: 21-MAY-1997
        CLASSIFICATION: 435
     PRIOR APPLICATION DATA:
        APPLICATION NUMBER:
        FILING DATE:
     ATTORNEY/AGENT INFORMATION:
        NAME: Field, Bret E.
        REGISTRATION NUMBER: 37,620
        REFERENCE/DOCKET NUMBER: 09096/002001
     TELECOMMUNICATION INFORMATION:
        TELEPHONE: 415-322-5070
        TELEFAX: 415-854-0875
     INFORMATION FOR SEQ ID NO: 1221:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 26 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
     MOLECULE TYPE: DNA
     FEATURE:
        OTHER INFORMATION: oligonucleotide primer
     SEQUENCE DESCRIPTION: SEQ ID NO: 1221:
US-08-859-998-1221

Query Match   3.3%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    64 TCCACCAGGCAGAAGATGACAGACTG 89
         ||||||||||||||||||||||||||
Db     1 TCCACCAGGCAGAAGATGACAGACTG 26
```

RESULT 4
US-09-225-928-1221
Sequence 1221, Application US/09225928
Patent No. 6352829
  GENERAL INFORMATION:
     APPLICANT: Chenchik, Alex
              Jokhadze, George
              Bibilashvilli, Robert
     TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
              EXPRESSION
     NUMBER OF SEQUENCES: 1375
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: Fish & Richardson, P.C.
        STREET: 2200 Sand Hill Road, Suite 100
        CITY: Menlo Park
        STATE: CA
        COUNTRY: US
        ZIP: 94025
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: Windows95
        SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:

```
~      APPLICATION NUMBER: US/09/225,928
~        FILING DATE: 05-Jan-1999
~      CLASSIFICATION: <Unknown>
~      PRIOR APPLICATION DATA:
~        APPLICATION NUMBER: 08/859,998
~        FILING DATE: 21-MAY-1997
~      ATTORNEY/AGENT INFORMATION:
~        NAME: Field, Bret E.
~        REGISTRATION NUMBER: 37,620
~        REFERENCE/DOCKET NUMBER: 09096/002001
~      TELECOMMUNICATION INFORMATION:
~        TELEPHONE: 415-322-5070
~        TELEFAX: 415-854-0875
~      INFORMATION FOR SEQ ID NO: 1221:
~        SEQUENCE CHARACTERISTICS:
~          LENGTH: 26 base pairs
~          TYPE: nucleic acid
~          STRANDEDNESS: single
~          TOPOLOGY: linear
~        MOLECULE TYPE: DNA
~        FEATURE:
~          OTHER INFORMATION: oligonucleotide primer
~        SEQUENCE DESCRIPTION: SEQ ID NO: 1221:
US-09-225-928-1221

Qy    64 TCCACCAGGCAGAAGAGATGACAGACTG 89
         ||||||||||||||||||||||||||||
Db     1 TCCACCAGGCAGAAGAGATGACAGACTG 26

Query Match     3.3%;  Score 26;  DB 4;  Length 26;
Best Local Similarity   100.0%;
Matches 26;  Conservative 0;  Pred. No. 0.00075;  Mismatches 0;  Indels 0;  Gaps 0;


RESULT 5
US-09-226-568-17/c
Sequence 17, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
~      APPLICANT: Ackermann, Elizabeth J.
~      APPLICANT: Bennett, C. Frank
~      APPLICANT: Dean, Nicholas M.
~      APPLICANT: Marcusson, Eric G.
~      TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
~      TITLE OF INVENTION: bcl-2-Related Proteins
~      FILE REFERENCE: ISPH-0337
~      CURRENT APPLICATION NUMBER: US/09/226,568
~      CURRENT FILING DATE: 1999-01-07
~      NUMBER OF SEQ ID NOS: 39
~      SOFTWARE: Patentin Ver. 2.0
~      SEQ ID NO 17
~        LENGTH: 22
~        TYPE: DNA
~        ORGANISM: Artificial Sequence
~        FEATURE:
~        OTHER INFORMATION: Description of Artificial Sequence: antisense
~        OTHER INFORMATION: sequence
US-09-226-568-17

Query Match     2.8%;  Score 22;  DB 3;  Length 22;
Best Local Similarity   100.0%;
Matches 22;  Conservative 0;  Pred. No. 0.081;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   663 ACGATTGCCAACACATACTTCT 684
         |||||||||||||||||||||||
Db    22 ACGATTGCCAACACATACTTCT 1


RESULT 6
US-09-226-568-2/c
Sequence 2, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
```

```
~      APPLICANT: Ackermann, Elizabeth J.
~      APPLICANT: Bennett, C. Frank
~      APPLICANT: Dean, Nicholas M.
~      APPLICANT: Marcusson, Eric G.
~      TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
~      TITLE OF INVENTION: bcl-2-Related Proteins
~      FILE REFERENCE: ISPH-0337
~      CURRENT APPLICATION NUMBER: US/09/226,568
~      CURRENT FILING DATE: 1999-01-07
~      NUMBER OF SEQ ID NOS: 39
~      SOFTWARE: Patentin Ver. 2.0
~      SEQ ID NO 2
~        LENGTH: 20
~        TYPE: DNA
~        ORGANISM: Artificial Sequence
~        FEATURE:
~        OTHER INFORMATION: Description of Artificial Sequence: antisense
~        OTHER INFORMATION: sequence
US-09-226-568-2

Qy    1 GAGTGAGCATTCTCAGCACA 20
        ||||||||||||||||||||
Db   20 GAGTGAGCATTCTCAGCACA 1

Query Match     2.6%;  Score 20;  DB 3;  Length 20;
Best Local Similarity   100.0%;
Matches 20;  Conservative 0;  Pred. No. 0.85;  Mismatches 0;  Indels 0;  Gaps 0;


RESULT 7
US-09-226-568-3/c
Sequence 3, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
~      APPLICANT: Ackermann, Elizabeth J.
~      APPLICANT: Bennett, C. Frank
~      APPLICANT: Dean, Nicholas M.
~      APPLICANT: Marcusson, Eric G.
~      TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
~      TITLE OF INVENTION: bcl-2-Related Proteins
~      FILE REFERENCE: ISPH-0337
~      CURRENT APPLICATION NUMBER: US/09/226,568
~      CURRENT FILING DATE: 1999-01-07
~      NUMBER OF SEQ ID NOS: 39
~      SOFTWARE: Patentin Ver. 2.0
~      SEQ ID NO 3
~        LENGTH: 20
~        TYPE: DNA
~        ORGANISM: Artificial Sequence
~        FEATURE:
~        OTHER INFORMATION: Description of Artificial Sequence: antisense
~        OTHER INFORMATION: sequence
US-09-226-568-3

Query Match     2.6%;  Score 20;  DB 3;  Length 20;
Best Local Similarity   100.0%;
Matches 20;  Conservative 0;  Pred. No. 0.85;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   19 CATTGCCTCAACACAGCTTCAA 38
        ||||||||||||||||||||||
Db   20 CATTGCCTCAACAGCTTCAA 1


RESULT 8
US-09-226-568-4/c
Sequence 4, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
~      APPLICANT: Ackermann, Elizabeth J.
~      APPLICANT: Bennett, C. Frank
~      APPLICANT: Dean, Nicholas M.
~      APPLICANT: Marcusson, Eric G.
~      TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
```

;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn Ver. 2.0

;   SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-226-568-4

Qy   39 GGTGAGCCAGCTCAAGACTT 58
               ||||||||||||||||||||
Db   20 GGTGAGCCAGCTCAAGACTT 1

Query Match   2.6%;   Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 9
US-09-226-568-5/c
;   Sequence 5, Application US/09226568
;   Patent No. 6001992
;   GENERAL INFORMATION:
;   APPLICANT: Ackermann, Elizabeth J.
;   APPLICANT: Bennett, C. Frank
;   APPLICANT: Dean, Nicholas M.
;   APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn Ver. 2.0

;   SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-226-568-5

Qy   66 CACCAGGCAGGAAGATGACAG 85
               ||||||||||||||||||||
Db   20 CACCAGGCAGGAAGATGACAG 1

Query Match   2.6%;   Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 10
US-09-226-568-6/c
;   Sequence 6, Application US/09226568
;   Patent No. 6001992
;   GENERAL INFORMATION:
;   APPLICANT: Ackermann, Elizabeth J.
;   APPLICANT: Bennett, C. Frank
;   APPLICANT: Dean, Nicholas M.
;   APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39

;   SOFTWARE: PatentIn Ver. 2.0

;   SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-226-568-6

Qy   91 GAATTTGGATATATTACAG 110
               ||||||||||||||||||||
Db   20 GAATTTGGATATATTACAG 1

Query Match   2.6%;   Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 11
US-09-226-568-7/c
;   Sequence 7, Application US/09226568
;   Patent No. 6001992
;   GENERAL INFORMATION:
;   APPLICANT: Ackermann, Elizabeth J.
;   APPLICANT: Bennett, C. Frank
;   APPLICANT: Dean, Nicholas M.
;   APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn Ver. 2.0

;   SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-226-568-7

Qy   111 GCTGGCTCAGGACTATCTGC 130
               ||||||||||||||||||||
Db   20 GCTGGCTCAGGACTATCTGC 1

Query Match   2.6%;   Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 12
US-09-226-568-8/c
;   Sequence 8, Application US/09226568
;   Patent No. 6001992
;   GENERAL INFORMATION:
;   APPLICANT: Ackermann, Elizabeth J.
;   APPLICANT: Bennett, C. Frank
;   APPLICANT: Dean, Nicholas M.
;   APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn Ver. 2.0

;   SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence

```
    FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: antisense
;     OTHER INFORMATION: sequence
US-09-226-568-8

Qy   193 AATGTTGCGTTCTCAGTCCA 212
         ||||||||||||||||||||
Db    20 AATGTTGCGTTCTCAGTCCA 1

Query Match    2.6%;    Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 13
US-09-226-568-9/c
Sequence 9, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
;     APPLICANT: Ackermann, Elizabeth J.
;     APPLICANT: Bennett, C. Frank
;     APPLICANT: Dean, Nicholas M.
;     APPLICANT: Marcusson, Eric G.
;     TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
;     TITLE OF INVENTION: bcl-2-Related Proteins
;     FILE REFERENCE: ISPH-0337
;     CURRENT APPLICATION NUMBER: US/09/226,568
;     CURRENT FILING DATE: 1999-01-07
;     NUMBER OF SEQ ID NOS: 39
;     SOFTWARE: Patentin Ver. 2.0
;     SEQ ID NO 9
;     LENGTH: 20
;     TYPE: DNA
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: antisense
;     OTHER INFORMATION: sequence
US-09-226-568-9
```

```
Query Match    2.6%;    Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   271 GACACTGCCAGAACACTATT 290
         ||||||||||||||||||||
Db    20 GACACTGCCAGAACACTATT 1

RESULT 14
US-09-226-568-10/c
Sequence 10, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
;     APPLICANT: Ackermann, Elizabeth J.
;     APPLICANT: Bennett, C. Frank
;     APPLICANT: Dean, Nicholas M.
;     APPLICANT: Marcusson, Eric G.
;     TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
;     TITLE OF INVENTION: bcl-2-Related Proteins
;     FILE REFERENCE: ISPH-0337
;     CURRENT APPLICATION NUMBER: US/09/226,568
;     CURRENT FILING DATE: 1999-01-07
;     NUMBER OF SEQ ID NOS: 39
;     SOFTWARE: Patentin Ver. 2.0
;     SEQ ID NO 10
;     LENGTH: 20
;     TYPE: DNA
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: antisense
;     OTHER INFORMATION: sequence
US-09-226-568-10
```

```
Query Match    2.6%;    Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   309 GGAGTTTGAAGACGGCATCA 328
         ||||||||||||||||||||
Db    20 GGAGTTTGAAGACGGCATCA 1

RESULT 15
US-09-226-568-11/c
Sequence 11, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
;     APPLICANT: Ackermann, Elizabeth J.
;     APPLICANT: Bennett, C. Frank
;     APPLICANT: Dean, Nicholas M.
;     APPLICANT: Marcusson, Eric G.
;     TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
;     TITLE OF INVENTION: bcl-2-Related Proteins
;     FILE REFERENCE: ISPH-0337
;     CURRENT APPLICATION NUMBER: US/09/226,568
;     CURRENT FILING DATE: 1999-01-07
;     NUMBER OF SEQ ID NOS: 39
;     SOFTWARE: Patentin Ver. 2.0
;     SEQ ID NO 11
;     LENGTH: 20
;     TYPE: DNA
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: antisense
;     OTHER INFORMATION: sequence
US-09-226-568-11
```

```
Query Match    2.6%;    Score 20;   DB 3;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 0.85;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   379 AAGAAACTTCTACGACAGCA 398
         ||||||||||||||||||||
Db    20 AAGAAACTCTTCACGACAGCA 1

Search completed: March 14, 2003, 08:31:49
Job time : 21.863 secs
```

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 07:14:05 ; Search time 49.143 Seconds
               (without alignments)
               11140.041 Million cell updates/sec

Title: US-09-869-894-1
Perfect score: 780
Sequence: 1 gagtgagcattctcagcaca..........aattgtatgtattttctct 780

Scoring table: OLIGO_NUC
               Gapop 60.0 , Gapext 60.0
               Gapop 60.0 , Gapext 60.0

Searched: 501302 seqs, 350925545 residues

Word size :   0

Total number of hits satisfying chosen parameters: 282380

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	1.8	20	9	US-09-834-721-6	Sequence 6, Appli
2	14	1.8	20	10	US-09-854-883-248	Sequence 248, App
3	14	1.8	20	10	US-09-752-639-24	Sequence 24, Appl
4	14	1.8	20	10	US-09-984-198-24	Sequence 24, Appl
5	14	1.8	20	10	US-09-951-536-6	Sequence 6, Appli
6	14	1.8	20	10	US-09-963-521-6	Sequence 6, Appli
7	14	1.8	25	10	US-09-398-399-34	Sequence 34, Appl
8	14	1.8	25	10	US-09-899-381-34	Sequence 34, Appl
9	14	1.8	27	10	US-09-804-690-17	Sequence 17, Appl
10	14	1.8	27	10	US-10-083-168-57	Sequence 57, Appl
11	14	1.8	30	6	US-10-092-140-4	Sequence 4, Appli
12	13	1.7	19	9	US-09-909-567B-35	Sequence 35, Appl
13	13	1.7	20	9	US-09-734-672-60	Sequence 60, Appl
14	13	1.7	20	9	US-09-982-828-60	Sequence 60, Appl
15	13	1.7	20	9	US-10-022-819-55	Sequence 55, Appl
16	13	1.7	20	10	US-09-800-631-81	Sequence 81, Appl
17	13	1.7	20	10	US-09-800-631-82	Sequence 82, Appl
18	13	1.7	21	9	US-09-892-398-44	Sequence 44, Appl
19	13	1.7	23	9	US-09-944-413-20	Sequence 20, Appl
20	13	1.7	23	9	US-09-944-403-20	Sequence 20, Appl
21	13	1.7	23	9	US-09-944-896-20	Sequence 20, Appl
22	13	1.7	23	9	US-09-944-944-20	Sequence 20, Appl
23	13	1.7	23	9	US-09-944-907-20	Sequence 20, Appl
24	13	1.7	23	9	US-09-944-929-20	Sequence 20, Appl
25	13	1.7	23	10	US-10-024-018-1	Sequence 1, Appl
26	13	1.7	23	10	US-09-841-366A-58	Sequence 58, Appl
27	13	1.7	23	10	US-09-866-028-20	Sequence 20, Appl
28	13	1.7	23	10	US-09-944-449-20	Sequence 20, Appl
29	13	1.7	23	10	US-09-944-457-20	Sequence 20, Appl
30	13	1.7	23	10	US-09-945-587-20	Sequence 20, Appl
31	13	1.7	23	10	US-09-945-015-20	Sequence 20, Appl
32	13	1.7	23	10	US-09-944-097-20	Sequence 20, Appl
33	13	1.7	23	10	US-09-944-432-20	Sequence 20, Appl
34	13	1.7	23	10	US-09-943-762-20	Sequence 20, Appl
35	13	1.7	23	10	US-09-944-654-20	Sequence 20, Appl
36	13	1.7	23	10	US-09-943-851A-20	Sequence 20, Appl
37	13	1.7	24	9	US-10-167-528-2	Sequence 2, Appli
38	13	1.7	24	10	US-09-860-793-16	Sequence 16, Appl
39	13	1.7	31	10	US-09-782-650-18	Sequence 18, Appl
40	13	1.7	31	10	US-09-782-650-19	Sequence 19, Appl
41	13	1.7	32	10	US-09-930-251-9	Sequence 9, Appli
42	13	1.7	42	9	US-10-206-654-1	Sequence 1, Appli
43	13	1.7	45	9	US-09-747-377-359	Sequence 359, App
44	13	1.7	45	9	US-09-992-598-192	Sequence 192, App
45	13	1.7	50	9	US-09-834-721-6	Sequence 20, App

ALIGNMENTS

RESULT 1
US-09-834-721-6/c
Sequence 6, Application US/09834721
Patent No. US20020155551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: primer
US-09-834-721-6

Query Match   100.0%; Score 14; DB 9; Length 20;
Best Local Similarity   100.0%;
Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   472 GAATGGATAAGGCA 485
              |||||||||||||
Db   17 GAATGGATAAGGCA 4

RESULT 2
US-09-854-883-248/c
Sequence 248, Application US/09854883
Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsert
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier

; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 248
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-854-883-248

Qy   300 GATGGAAAAGGAGT 313
          ||||||||||||||
Db   14 GATGGAAAAGGAGT 1

Query Match   1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-752-639-24/c
Sequence 24, Application US09752639
Patent No. US20020091243A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-752-639-24

Query Match   1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   341 GAATTGTAACCATA 354
          ||||||||||||||
Db   20, GAATTGTAACCATA 7

RESULT 4
US-09-984-198-24/c
Sequence 24, Application US09984198
Patent No. US20020106679A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-984-198-24

Query Match   1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   341 GAATTGTAACCATA 354
         ||||||||||||||
Db    20 GAATTGTAACCATA 7
```

RESULT 5
US-09-951-536-6/c
Sequence 6, Application US/00951536
Patent No. US20020107378A1
GENERAL INFORMATION:
;   APPLICANT: ZIEGLER, PETRA
;   APPLICANT: EGGELING, LOTHAR
;   APPLICANT: SAHM, HERMANN
;   APPLICANT: THIERBACH, GEORG
;   TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
;   TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;   TITLE OF INVENTION: USING CORYNEFORM BACTERIA
;   FILE REFERENCE: 21123/28214/MAS
;   CURRENT APPLICATION NUMBER: US/09/951,536
;   CURRENT FILING DATE: 2001-09-14
;   PRIOR APPLICATION NUMBER: 09/431,099
;   PRIOR FILING DATE: 1999-11-01
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-951-536-6

Query Match   1.8%; Score 14; DB 10; Length 20;
Best Local Similarity   100.0%; Pred. No. 1.8e+03;
Matches   14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   472 GAATGGATAAGGCA 485
         ||||||||||||||
Db    17 GAATGGATAAGGCA 4
```

RESULT 6
US-09-963-521-6/c
Sequence 6, Application US/09963521
Patent No. US20020146781A1
GENERAL INFORMATION:
;   APPLICANT: ZIEGLER, PETRA
;   APPLICANT: EGGELING, LOTHAR
;   APPLICANT: SAHM, HERMANN
;   TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
;   TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
;   TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
;   FILE REFERENCE: 21123/28413/MAS
;   CURRENT APPLICATION NUMBER: US/09/963,521
;   CURRENT FILING DATE: 2001-09-27
;   PRIOR APPLICATION NUMBER: 09/431,099
;   PRIOR FILING DATE: 1999-11-01
;   PRIOR APPLICATION NUMBER: DE 199 41 478.5
;   PRIOR FILING DATE: 1999-09-01
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-963-521-6

Query Match   1.8%; Score 14; DB 10; Length 20;
Best Local Similarity   100.0%; Pred. No. 1.8e+03;
Matches   14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   472 GAATGGATAAGGCA 485
         ||||||||||||||
Db    17 GAATGGATAAGGCA 4
```

RESULT 7
US-09-398-399-34
Sequence 34, Application US/09398399
Patent No. US20020051973A1
GENERAL INFORMATION:
;   APPLICANT: DELENSTARR, GLENDA C.
;   APPLICANT: LEFKOWITZ, STEVEN M.
;   APPLICANT: LUEBKE, KEVIN J.
;   APPLICANT: OVERMAN, LESLIE B.
;   APPLICANT: SAMPRAS, NICHOLAS M.
;   APPLICANT: SAMPSON, JEFFREY R.
;   APPLICANT: WOLBER, PAUL K.
;   TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC
;   TITLE OF INVENTION: ACIDS TO SURFACES
;   FILE REFERENCE: 10981620-1
;   CURRENT APPLICATION NUMBER: US/09/398,399
;   CURRENT FILING DATE: 1999-09-17
;   NUMBER OF SEQ ID NOS: 35
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 34
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-398-399-34

Query Match   1.8%; Score 14; DB 10; Length 25;
Best Local Similarity   100.0%; Pred. No. 1.8e+03;
Matches   14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   531 ATCTGGCTGGATGA 544
         ||||||||||||||
Db    12 ATCTGGCTGGATGA 25
```

RESULT 8
US-09-899-381-34
Sequence 34, Application US/09899381
Patent No. US20020068293A1
GENERAL INFORMATION:
;   APPLICANT: Delenstarr, Glend C.
;   APPLICANT: Wolber, Pual K.
;   APPLICANT: Sana, Theodore R.
;   TITLE OF INVENTION: Arrays Having Background Features and
;   TITLE OF INVENTION: Methods for Using the Same
;   FILE REFERENCE: 10010760-1
;   CURRENT APPLICATION NUMBER: US/09/899,381
;   CURRENT FILING DATE: 2001-07-05
;   PRIOR APPLICATION NUMBER: 09/398,399
;   PRIOR FILING DATE: 1999-09-17
;   NUMBER OF SEQ ID NOS: 53
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 34
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic probe
US-09-899-381-34

Query Match   1.8%; Score 14; DB 10; Length 25;
Best Local Similarity   100.0%; Pred. No. 1.8e+03;
Matches   14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   531 ATCTGGCTGGATGA 544
         ||||||||||||||
Db    12 ATCTGGCTGGATGA 25
```

RESULT 9
US-10-083-168-57
Sequence 57, Application US/10083168
Publication No. US20030023069A1
GENERAL INFORMATION:
APPLICANT: Liaw, Chen W.
APPLICANT: Chalmers, Derek T.
APPLICANT: Behan, Dominic P.
APPLICANT: Maciejewski-Lenior, Dominique
APPLICANT: Leonard, James N.
APPLICANT: Ortuno, Daniel
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0320
CURRENT APPLICATION NUMBER: US/10/083,168
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
SEQ ID NO 57
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: No. US20030023069Alel Sequence

Query Match   1.8%;   Score 14; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   42 GAGCCAGCTCAAGA 55
         ||||||||||||||
Db   3 GAGCCAGCTCAAGA 16

RESULT 10
US-09-804-690-17
Sequence 17, Application US/09804690
Patent No. US2002003474 3A1
GENERAL INFORMATION:
APPLICANT: LI, Limin
APPLICANT: COHEN, Stanley N
TITLE OF INVENTION: MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND THEIR USES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH AND RICHARDSON, P.C.
 STREET: 2200 SAND HILL ROAD
 CITY: MENLO PARK
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/804,690
 FILING DATE: 12-Mar-2001
 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/146,187
 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
 NAME: SHERWOOD, Pamela J.
 REGISTRATION NUMBER: 36,677
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249

  TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 27 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
  DESCRIPTION: /desc = "Primer"
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-804-690-17

Query Match   1.8%;   Score 14; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   42 GAGCCAGCTCAAGA 55
         ||||||||||||||
Db   12 GAGCCAGCTCAAGA 25

RESULT 11
US-10-092-140-4
Sequence 4, Application US/10092140
Patent No. US20020164801A1
GENERAL INFORMATION:
APPLICANT: McGill University et al.
TITLE OF INVENTION: HUMAN AND MAMMALIAN DNA
        REPLICATION ORIGIN CONSENSUS SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
 ADDRESSEE: SWABEY OGILVY RENAULT
 STREET: 1981 McGill College Avenue - Suite 1600
 CITY: Montr.al
 STATE: QC
 COUNTRY: Canada
 ZIP: H3A 2Y3
COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/092,140
 FILING DATE: 06-Mar-2002
 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/328,750
 FILING DATE: 09-Jun-1999
 APPLICATION NUMBER: 60/033,374
 FILING DATE: 16-DEC-1996
 APPLICATION NUMBER: 60/047,322
 FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
 NAME: C"t., France
 REGISTRATION NUMBER: 4166
 REFERENCE/DOCKET NUMBER: 1770-162PCT FC/1d
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 514 845-7126
 TELEFAX: 514 288-8389
 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 30 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-092-140-4

Query Match   1.8%;   Score 14; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   431 TTTCATATTTTGTT 444
          ||||||||||||||
Db   8 TTTCATATTTGTT 21

RESULT 12
US-09-909-567B-35
Sequence 35, Application US/09909567B
Publication No. US20030022257A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto A.
APPLICANT: Nair, Manoj
APPLICANT: Chen, Selyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1

SEQ ID NO 35
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-909-567B-35

Query Match   1.7%; Score 13; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches   13; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   535 GGCTGGATGACTT 547
          |||||||||||||
Db   3 GGCTGGATGACTT 15

RESULT 13
US-09-734-672-60/c
Sequence 60, Application US/09734672
Publication No. US20020183268A1
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
          Alvares, Christopher P.
          Critz, Brenda S.
          Olson, Sheri J.
          Schelter, Denise B.
          Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
                    BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Ave., N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,672
FILING DATE: 03-Dec-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/966,436
FILING DATE: 07-No. US20020183268A1-97

APPLICATION NUMBER: US 08/598,591
FILING DATE: 12-Feb-96
ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44921-5055-02-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20020183268A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: 18R primer
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-734-672-60

Query Match   1.7%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches   13; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   494 GCTGGGAAAATGG 506
          |||||||||||||
Db   17 GCTGGGAAAATGG 5

RESULT 14
US-09-982-828-60/c
Sequence 60, Application US/09982828
Publication No. US20030022184A1
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
          Alvares, Christopher P.
          Critz, Brenda S.
          Olson, Sheri J.
          Thurber, Denise
          Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
                    BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,828
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/074,453
FILING DATE: 1998-05-06
APPLICATION NUMBER: US 08/798,691
FILING DATE: 1997-02-12
APPLICATION NUMBER: US 08/598,591
FILING DATE: 1996-02-12
ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44921-5053-01-US
TELECOMMUNICATION INFORMATION:

RESULT 15
US-10-022-819-55/c
Sequence 55, Application US/10022819
Publication No. US20030027166A1
GENERAL INFORMATION:
APPLICANT: ALLEN, Antoinette C. P.
OLSEN, Sheri J.
LAWRENCE, Tammy
ANGELLY, Tracy S.
RABIN, Mark B.
TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
BRCA1 GENE
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue
CITY: Washington DC
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/022,819
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,452
FILING DATE: 1998-05-06
ATTORNEY/AGENT INFORMATION:
NAME: <Unknown>
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 044921-5049-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-022-819-55

Query Match   1.7%; Score 13; DB 9; Length 20;
Best Local Similarity   100.0%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   494 GCTGGGGAAAATGG 506
           ||||||||||||||
Db   17 GCTGGGGAAAATGG   5

Search completed: March 14, 2003, 10:59:22
Job time : 49.143 secs

TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: 18R primer
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-982-828-60

Query Match   1.7%; Score 13; DB 9; Length 20;
Best Local Similarity   100.0%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   494 GCTGGGGAAAATGG 506
           ||||||||||||||
Db   17 GCTGGGGAAAATGG   5

OM nucleic - nucleic search, using sw model

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 03:41:43 ; Search time 114.171 Seconds

Title: US-09-869-894-1
Perfect score: 780
Sequence: 1 gagtgaagcattccaagcaca............aattgtatgtatttctct 780

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0
                 15385.391 Million cell updates/sec

Searched: 2185239 seqs, 112599159 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_101002:*

```
 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
```

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
c 1	28	3.6	28	24	ABK67134	Human gene specifi
c 2	26	3.3	24	24	ABK67133	Human gene specifi
c 3	22	2.8	22	22	AA239089	Human A1 anti-apop
c 4	20	2.6	20	16	AAT41123	Human gene signatu
c 5	20	2.6	20	16	AAT41124	Human gene signatu
c 6	20	2.6	20	21	AA239069	Human A1 anti-apop
c 7	20	2.6	20	21	AA239070	Human A1 anti-apop
c 8	20	2.6	20	21	AA239071	Human A1 anti-apop
c 9	20	2.6	20	21	AA239072	Human A1 anti-apop
c 10	20	2.6	20	21	AA239073	Human A1 anti-apop
c 11	20	2.6	20	21	AA239074	Human A1 anti-apop
c 12	20	2.6	20	21	AA239075	Human A1 anti-apop
c 13	20	2.6	20	21	AA239076	Human A1 anti-apop
c 14	20	2.6	20	21	AA239077	Human A1 anti-apop
c 15	20	2.6	20	21	AA239078	Human A1 anti-apop
c 16	20	2.6	20	21	AA239079	Human A1 anti-apop
c 17	20	2.6	20	21	AA239080	Human A1 anti-apop
c 18	20	2.6	20	21	AA239081	Human A1 anti-apop
c 19	20	2.6	20	21	AA239082	Human A1 anti-apop
c 20	20	2.6	20	21	AA239088	Human A1 anti-apop
c 21	20	2.1	22	17	AAT16171	Primer #1 for huma
c 22	20	2.1	24	24	AA196409	Primer used to amp
c 23	15	1.9	24	24	ABL40366	Primer 2 relative
c 24	15	1.9	32	20	AA161446	Human PTB1B protei
c 25	15	1.9	38	20	AA209965	Human PTP1b forward PCR
c 26	15	1.9	42	46	AAF76697	Human PTP1b coding
c 27	15	1.9	46	16	AAT25577	Human gene signatu
c 28	14	1.8	19	19	AAA86392	PCBA HH ribozyme b
c 29	14	1.8	19	19	AAA86393	PCBA HH ribozyme b
c 30	14	1.8	19	19	AAA86394	PCBA HH ribozyme b
c 31	14	1.8	19	21	AAA86395	PCBA HH ribozyme b
c 32	14	1.8	19	21	AAA86396	PCBA HH ribozyme b
c 33	14	1.8	19	21	AAH61554	PCNA HH ribozyme b
c 34	14	1.8	19	22	AAH61555	PCNA HH ribozyme b
c 35	14	1.8	19	22	AAH61556	PCNA HH ribozyme b
c 36	14	1.8	19	22	AAH61557	PCNA HH ribozyme b
c 37	14	1.8	19	22	AAH61558	PCNA HH ribozyme b
c 38	14	1.8	20	22	AAZ17990	PCNA HH ribozyme b
c 39	14	1.8	20	21	AAZ17886	PCNA HH ribozyme b
c 40	14	1.8	20	20	AAZ44575	Homeobox conserved
c 41	14	1.8	20	21	AAH21118	Newcastle disease
c 42	14	1.8	20	22	AAF61241	C. glutamicum brnF
c 43	14	1.8	20	22	AAC86402	C. glutamicum tran
c 44	14	1.8	20	22	AAC86403	Human bcl-2 mRNA n
c 45	14	1.8	20	22	AAC86405	Human bcl-XL and b

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
ABK67134/c
ID   ABK67134 standard; DNA; 28 BP.
XX
AC   ABK67134;
XX
DT   02-JUL-2002 (first entry)
XX
DE   Human gene specific PCR primer #1222.
XX
KW   Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS   Homo sapiens.
XX
XX
PN   US6352829-B1.
XX
PD   05-MAR-2002.
XX
PF   05-JAN-1999;   99US-0225928.
XX
PR   21-MAY-1997;   97US-0859998.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Chenchik A,   Jokhadze G,   Bibilashvilli R;
XX
DR   WPI; 2002-314699/35.
XX
PT   Producing sub-population of labeled nucleic acids, useful for analysing
PT   differences in RNA profiles between several different physiological
PT   sources, using set of distinct gene specific primers

PS
XX
XX   Example 3; SEQ ID No 1222; 11pp; English.
CC   The invention relates to producing a sub-population of labeled nucleic
CC   acids (NAs) comprising contacting a NA sample from a physiological
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where
CC   each gene specific primer has a sequence complementary to a distinct
CC   mRNA, and each labeled NA is generated using a single gene specific
CC   primer. The method is useful for producing a sub-population of labeled
CC   NAs which is useful for analysing the differences in the RNA profiles
CC   between several different physiological sources, where the method
CC   comprises producing subpopulation of labeled NAs for the different
CC   physiological sources, comprising the populations for each physiological
CC   source to identify differences in the population, where the comparison
CC   is preferably performed by hybridising the labeled NAs for each of the
CC   distinct physiological sources to an array of probe NAs stably
CC   associated with the surface of a substrate to produce a hybridisation
CC   pattern for each of the sources, and comparing the patterns for each of
CC   the sources, where differential gene expression assays are
CC   utilised in differential expression analysis of diseased a normal
CC   tissue e.g. neoplastic a normal tissue, or different tissue or
CC   subtissue types. The present sequence is a human gene specific PCR
CC   primer used in the method of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from USPTO at
CC   http://www.seqdata.uspto.gov/sequence.html?DocID=6352829B1.
XX
SQ   Sequence 28 BP; 6 A; 4 C; 9 G; 9 T; 0 other;

Query Match   3.6%; Score 28; DB 24; Length 28;
Best Local Similarity   100.0%; Pred. No. 0.00074;
Matches   28; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   265 TCCGTAGACACTGCCAGAACACTATTCA 292
              ||||||||||||||||||||||||||||
Db   28 TCCGTAGACACTGCCAGAACACTATTCA 1

RESULT 2
ID   ABK67133 standard; DNA; 26 BP.
XX
AC   ABK67133;
XX
DT   02-JUL-2002 (first entry)
XX
DE   Human gene specific PCR primer #1221.
XX
KW   Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS   Homo sapiens.
XX
PN   US6352829-B1.
XX
PD   05-MAR-2002.
XX
PF   05-JAN-1999; 99US-0225928.
XX
PR   21-MAY-1997; 97US-0859998.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Chenchik A, Jokhadze G, Bibilashvilli R;
XX
DR   WPI; 2002-314699/35.
XX
PT   Producing sub-population of labeled nucleic acids, useful for analysing
PT   differences in RNA profiles between several different physiological
PT   sources, using set of distinct gene specific primers -
XX
PS   Example 3; SEQ ID No 1221; 11pp; English.

CC   The invention relates to producing a sub-population of labeled nucleic
CC   acids (NAs) comprising contacting a NA sample from a physiological
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where
CC   each gene specific primer has a sequence complementary to a distinct
CC   mRNA, and each labeled NA is generated using a single gene specific
CC   primer. The method is useful for producing a sub-population of labeled
CC   NAs which is useful for analysing the differences in the RNA profiles
CC   between several different physiological sources, where the method
CC   comprises producing subpopulation of labeled NAs for the different
CC   physiological sources, comprising the populations for each physiological
CC   source to identify differences in the population, where the comparison
CC   is preferably performed by hybridising the labeled NAs for each of the
CC   distinct physiological sources to an array of probe NAs stably
CC   associated with the surface of a substrate to produce a hybridisation
CC   pattern for each of the sources, and comparing the patterns for each of
CC   the sources, where differential gene expression assays are
CC   utilised in differential expression analysis of diseased a normal
CC   tissue e.g. neoplastic a normal tissue, or different tissue or
CC   subtissue types. The present sequence is a human gene specific PCR
CC   primer used in the method of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from USPTO at
CC   http://www.seqdata.uspto.gov/sequence.html?DocID=6352829B1.
XX
SQ   Sequence 26 BP; 9 A; 7 C; 7 G; 3 T; 0 other;

Query Match   3.3%; Score 26; DB 24; Length 26;
Best Local Similarity   100.0%; Pred. No. 0.0076;
Matches   26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   64 TCCACCAGGCGAAGAGATGACAGACTG 89
              |||||||||||||||||||||||||||
Db   1 TCCACCAGGCGAAGAGATGACAGACTG 26

RESULT 3
ID   AAZ39089 standard; DNA; 22 BP.
XX
AC   AAZ39089;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein PCR probe.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; PCR; probe; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999; 99US-0226568.
XX
PR   07-JAN-1999; 99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Example 9; Column 28; 28pp; English.

CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents a PCR probe for the human A1 nucleotide
CC   sequence.
XX
SQ   Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 other;

      Query Match   2.8%;   Score 22; DB 21; Length 22;
      Best Local Similarity 100.0%;   Pred. No. 0.79;
      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   663 ACGAATTGCCAACACATACTTCT 684
            ||||||||||||||||||||||
Db   22 ACGAATTGCCAACACATACTTCT 1

RESULT 4
AAT41123
ID   AAT41123 standard; DNA; 20 BP.
XX
AC   AAT41123;
XX
DT   03-DEC-1996   (first entry)
XX
DE   Human gene signature HUMGS01288-derived sense primer.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; primer; PCR; amplification;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K, Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Example 7; Fig 7; 2245pp; Japanese.
XX
CC   Primers T41001-T41382 are derived from novel human gene signature (GS)
CC   sequences which did not match with sequences deposited in Genbank release
CC   76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC   libraries prepared from various human tissues; synthesis of cDNA was
CC   initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC   Each library is constructed so as to reflect accurately the relative
CC   abundance of different mRNAs in the particular tissue from which it was
CC   derived. The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS sequences)

CC   as a means of diagnosing abnormal cell function or for recognising
CC   different cell types. The primers T41123-4 amplify clone pm2245 which
CC   comprises the GS HUMGS01288 (T20288), located on chromosome 10.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 other;

      Query Match   2.8%;   Score 20; DB 16; Length 20;
      Best Local Similarity 100.0%;   Pred. No. 8.1;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   571 TGTGAAATGCTATCTCTCCT 590
            ||||||||||||||||||||
Db   1 TGTGAAATGCTATCTCTCCT 20

RESULT 5
AAT41124/c
ID   AAT41124 standard; DNA; 20 BP.
XX
AC   AAT41124;
XX
DT   03-DEC-1996   (first entry)
XX
DE   Human gene signature HUMGS01288-derived anti-sense primer.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; primer; PCR; amplification;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K, Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Example 7; Fig 7; 2245pp; Japanese.
XX
CC   Primers T41001-T41382 are derived from novel human gene signature (GS)
CC   sequences which did not match with sequences deposited in Genbank release
CC   76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC   libraries prepared from various human tissues; synthesis of cDNA was
CC   initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC   Each library is constructed so as to reflect accurately the relative
CC   abundance of different mRNAs in the particular tissue from which it was
CC   derived. The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS sequences)
CC   as a means of diagnosing abnormal cell function or for recognising
CC   different cell types. The primers T41123-4 amplify clone pm2245 which
CC   comprises the GS HUMGS01288 (T20288), located on chromosome 10.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 other;

      Query Match   2.6%;   Score 20; DB 16; Length 20;
      Best Local Similarity 100.0%;   Pred. No. 8.1;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    651 ACTGATATGGAAACGATTGC 670
          ||||||||||||||||||||
Db     20 ACTGATATGGAAACGATTGC 1
```

RESULT 6
```
ID   AAZ39069/c
Db   AAZ39069 standard; DNA; 20 BP.
XX
AC   AAZ39069;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17484.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;  99US-0226568.
XX
PR   07-JAN-1999;  99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
XX
SQ   Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 other;
XX
XX
```

```
Query Match             100.0%;  Score 20;  DB 21;  Length 20;
Best Local Similarity   100.0%;
  Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    19 CATTGCCTCAACAGCTTCAA 38
         ||||||||||||||||||||
Db    20 CATTGCCTCAACAGCTTCAA 1
```

RESULT 7
```
ID   AAZ39070/c
Db   AAZ39070 standard; DNA; 20 BP.
XX
AC   AAZ39070;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17485.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;  99US-0226568.
XX
PR   07-JAN-1999;  99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
XX
SQ   Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;
XX
XX
```

```
Query Match             100.0%;  Score 20;  DB 21;  Length 20;
Best Local Similarity   100.0%;
  Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    39 GGTGAGCCAGCTCAAGACTT 58
         ||||||||||||||||||||
Db    20 GGTGAGCCAGCTCAAGACTT 1
```

RESULT 8
```
ID   AAZ39071/c
Db   AAZ39071 standard; DNA; 20 BP.
XX
AC   AAZ39071;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17486.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
```

RESULT 9
ID   AAZ39072/c
AAZ39072/c AAZ39072 standard; DNA; 20 BP.
XX
AC   AAZ39072;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17487.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999; 99US-0226568.
XX
PR   07-JAN-1999; 99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PS   Claim 21; Column 27; 28pp; English.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 other;

Query Match   2.68%; Score 20; DB 21; Length 20;
Best Local Similarity   100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   66 CACCAGGCGAAGAGATGACAG 85
        |||||||||||||||||||||
Db   20 CACCAGGCGAAGAGATGACAG 1

RESULT 10
ID   AAZ39073/c
AAZ39073/c AAZ39073 standard; DNA; 20 BP.
XX
AC   AAZ39073;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17488.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999; 99US-0226568.
XX
PR   07-JAN-1999; 99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PS   Claim 21; Column 27; 28pp; English.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in

SQ   Sequence 20 BP; 8 A; 4 C; 1 G; 7 T; 0 other;

Query Match   2.68%; Score 20; DB 21; Length 20;
Best Local Similarity   100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   91 GAATTTGGATATATTTACAG 110
        ||||||||||||||||||||
Db   20 GAATTTGGATATATTTACAG 1

```
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 other;

Qy          Query Match       100.0%;  Score 20;  DB 21;  Length 20;
            Best Local Similarity   2.6%;   Pred. No. 8.1;
            Matches 20;   Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   111 GCTGGCTCAGGACTATCTGC 130
         ||||||||||||||||||||
Db    20 GCTGGCTCAGGACTATCTGC 1
```

RESULT 11

```
ID   AA239074/c
AC   AA239074/c
XX
AC   AA239074;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17489.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;  99US-0226568.
XX
PR   07-JAN-1999;  99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;
```

RESULT 12

```
Qy          Query Match       100.0%;  Score 20;  DB 21;  Length 20;
            Best Local Similarity   2.6%;   Pred. No. 8.1;
            Matches 20;   Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   193 AATGTTGCGTTCTCAGTCCA 212
         ||||||||||||||||||||
Db    20 AATGTTGCGTTCTCAGTCCA 1

ID   AA239075/c
AC   AA239075/c
XX
AC   AA239075;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17490.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;  99US-0226568.
XX
PR   07-JAN-1999;  99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 other;
```

RESULT 13

```
Qy          Query Match       100.0%;  Score 20;  DB 21;  Length 20;
            Best Local Similarity   2.6%;   Pred. No. 8.1;
            Matches 20;   Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   271 GACACTGCCAGAACACTATT 290
         ||||||||||||||||||||
Db    20 GACACTGCCAGAACACTATT 1

ID   AA239076/c
AC   AA239076/c
XX
AC   AA239076;
XX
```

DT   29-FEB-2000 (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17491.
XX
KW   Human; A1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
DR   WPI; 2000-061908/05.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 other;

Query Match   2.6%; Score 20; DB 21; Length 20;
Best Local Similarity   100.0%;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   309 GGAGTTTGAAGACGGCATCA 328
          ||||||||||||||||||||
Db   20 GGAGTTTGAAGACGGCATCA 1

RESULT 14
AA239077/c
ID   AA239077 standard; DNA; 20 BP.
XX
AC   AA239077;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17492.
XX
KW   Human; A1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001992-A.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PD   14-DEC-1999.
XX
DR   WPI; 2000-061908/05.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 other;

Query Match   2.6%; Score 20; DB 21; Length 20;
Best Local Similarity   100.0%;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   379 AAGAAACTTCTACGACAGCA 398
          ||||||||||||||||||||
Db   20 AAGAAACTTCTACGACACCA 1

RESULT 15
AA239078/c
ID   AA239078 standard; DNA; 20 BP.
XX
AC   AA239078;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17493.
XX
KW   Human; A1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001992-A.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PD   14-DEC-1999.
XX
DR   WPI; 2000-061908/05.

XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 21; Column 27; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human A1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 other;

Query Match   2.6%;   Score 20;   DB 21;   Length 20;
Best Local Similarity   100.0%;   Pred. No. 8.1;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   556 GTTACAGGAAAGATCTGTGA 575
           ||||||||||||||||||||
Db   20 GTTACAGGAAAGATCTGTGA 1

Search completed: March 14, 2003, 04:46:51
Job time : 117.671 secs

OM nucleic - nucleic search, using sw model

Run on: GenCore version 5.1.4_p5_4578
                                 Copyright (c) 1993 - 2003 Compugen Ltd.

                                 March 14, 2003, 04:35:16 ; Search time 1148.99 Seconds
                                 (without alignments)
                                 17066.215 Million cell updates/sec

Title: US-09-869-894-1
Perfect score: 780
Sequence: 1 gagtgagcattctcaagcaca..........aattgtatgtattttctct 780

Scoring table: OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size :   0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   Pending_Patents_NA_Main:*

1:   /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
2:   /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
3:   /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
4:   /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
5:   /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
6:   /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
7:   /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
8:   /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
9:   /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
44: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US6008_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US6023_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
84: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
85: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	50	50	1	PCT-US01-47856-2596	Sequence 2596, App
2	50	50	50	1	PCT-US01-47856-3838	Sequence 3838, App
3	50	6.4	50	40	US-10-131-827-2596	Sequence 2596, App
4	50	6.4	50	40	US-10-131-827-3838	Sequence 3838, Ap
5	50	6.4	50	40	US-10-131-827-2596	Sequence 2596, Ap
6	50	6.4	50	40	US-10-131-831-2596	Sequence 2596, Ap
7	28	3.6	28	16	US-10-131-831-3838	Sequence 3838, Ap
8	26	3.3	26	16	US-09-225-201B-1222	Sequence 1222, Ap
9	22	2.8	22	1	US-09-225-201B-1221	Sequence 1221, Ap
10	22	2.8	22	33	US-09-869-894-17	Sequence 17, Appl
11	22	2.8	22	1	US-09-869-894-17	Sequence 17, Appl
12	20	2.6	20	1	PCT-US99-29593-17	Sequence 2, Appl
13	20	2.6	20	1	PCT-US99-29593-2	Sequence 3, Appl
14	20	2.6	20	1	PCT-US99-29593-3	Sequence 3838, Ap
15	20	2.6	20	1	PCT-US99-29593-4	Sequence 4, Appl
16	20	2.6	20	1	PCT-US99-29593-5	Sequence 5, Appl
17	20	2.6	20	1	PCT-US99-29593-6	Sequence 6, Appl
18	20	2.6	20	1	PCT-US99-29593-7	Sequence 7, Appl
19	20	2.6	20	1	PCT-US99-29593-8	Sequence 8, Appl
20	20	2.6	20	1	PCT-US99-29593-9	Sequence 9, Appl
21	20	2.6	20	1	PCT-US99-29593-10	Sequence 10, Appl
19	20	2.6	20	1	PCT-US99-29593-11	Sequence 11, Appl
20	20	2.6	20	1	PCT-US99-29593-12	Sequence 12, Appl

```
c  22  20  2.6   1   PCT-US99-29593-13     Sequence 13, Appl
c  23  20  2.6   1   PCT-US99-29593-14     Sequence 14, Appl
c  24  20  2.6   1   PCT-US99-29593-15     Sequence 15, Appl
c  25  20  2.6   1   PCT-US99-29593-16     Sequence 16, Appl
c  26  20  2.6  33   US-09-869-894-2       Sequence 2, Appli
c  27  20  2.6  33   US-09-869-894-3       Sequence 3, Appli
c  28  20  2.6  33   US-09-869-894-4       Sequence 4, Appli
c  29  20  2.6  33   US-09-869-894-5       Sequence 5, Appli
c  30  20  2.6  33   US-09-869-894-6       Sequence 6, Appli
c  31  20  2.6  33   US-09-869-894-7       Sequence 7, Appli
c  32  20  2.6  33   US-09-869-894-8       Sequence 8, Appli
c  33  20  2.6  33   US-09-869-894-9       Sequence 9, Appli
c  34  20  2.6  33   US-09-869-894-10      Sequence 10, Appl
c  35  20  2.6  33   US-09-869-894-11      Sequence 11, Appl
c  36  20  2.6  33   US-09-869-894-12      Sequence 12, Appl
c  37  20  2.6  33   US-09-869-894-13      Sequence 13, Appl
c  38  20  2.6  33   US-09-869-894-14      Sequence 14, Appl
c  39  20  2.6  33   US-09-869-894-15      Sequence 15, Appl
c  40  20  2.6  33   US-09-869-894-16      Sequence 16, Appl
c  41  17  2.2  18   US-09-404-520-41805   Sequence 41805, A
c  42  17  2.2  45   US-08-278-774-28      Sequence 28, Appl
c  42  16  2.1   6   US-09-396-196F-36231  Sequence 36231, A
c  43  16  2.1  25   US-09-396-196G-36231  Sequence 36231, A
c  44  16  2.1  17   US-09-954-427-70874   Sequence 70874, A
c  45  16  2.1  36
```

RESULT 1
PCT-US01-47856-2596
; Sequence 2596, Application PCT/US0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Quertermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 50661200140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2596
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47856-2596

ALIGNMENTS

; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Quertermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 50661200140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3838
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47856-3838

Query Match 100.0%; Score 50; DB 1; Length 50;
Best Local Similarity 6.4%; Pred. No. 7.7e-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50
```

RESULT 3
US-10-131-827-2596
; Sequence 2596, Application US/10131827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2596
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2596

Query Match 100.0%; Score 50; DB 1; Length 50;
Best Local Similarity 6.4%; Pred. No. 7.7e-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50
```

RESULT 2
PCT-US01-47856-3838
; Sequence 3838, Application PCT/US0147856
; GENERAL INFORMATION:

RESULT 4
US-10-131-827-3838
; Sequence 3838, Application US/10131827
; GENERAL INFORMATION:

GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3838
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-3838

Qy   703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50

Query Match   100.0%; Score 50; DB 40; Length 50;
Best Local Similarity 6.4%; Pred. No. 7.7e-16;
Matches   50; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 5
US-10-131-831-2596
Sequence 2596, Application US/1031831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 50661200121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2596
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2596

Qy   703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50

Query Match   100.0%; Score 50; DB 40; Length 50;
Best Local Similarity 6.4%; Pred. No. 7.7e-16;
Matches   50; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 6
US-10-131-831-3838
Sequence 3838, Application US/1031831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 50661200121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US/10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3838
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-3838

Qy   703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50

Query Match   100.0%; Score 50; DB 40; Length 50;
Best Local Similarity 6.4%; Pred. No. 7.7e-16;
Matches   50; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 7
US-09-225-201B-1222/c
Sequence 1222, Application US/092252201B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1222:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 1222:
US-09-225-201B-1222

Qy   703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50

Query Match   100.0%; Score 50; DB 40; Length 50;
Best Local Similarity 6.4%; Pred. No. 7.7e-16;
Matches   50; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 8
US-09-225-201B-1221
Sequence 1221, Application US/09225201B
GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 1221:
US-09-225-201B-1221

Query Match   3.3%;   Score 26;   DB 16;   Length 26;
Best Local Similarity   100.0%;   Pred. No. 0.011;
Matches   26;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   64   TCCACCAGGCCAGAAGATGACAGACTG   89
             ||||||||||||||||||||||||||
Db   1   TCCACCAGGCCAGAAGATGACAGACTG   26

RESULT 9
PCT-US99-29593-17/c
Sequence 17, Application PC/TUS9929593
GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.

Qy   265   TCCGTAGACACTGCCAGACACATTATTCA   292
              |||||||||||||||||||||||||||||
Db   28   TCCGTAGACACTGCCAGAACACTTATTCA   1

Query Match   3.6%;   Score 28;   DB 16;   Length 28;
Best Local Similarity   100.0%;   Pred. No. 0.00089;
Matches   28;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-17

Qy   663   ACGATTGCCAACACATACTTCT   684
              ||||||||||||||||||||||
Db   22   ACGATTGCCAACACATACTTCT   1

Query Match   2.8%;   Score 22;   DB 1;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 1.7;
Matches   22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 10
US-09-869-894-17/c
Sequence 17, Application US/09869894
GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: US/09/869,894
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 09/226,568
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
US-09-869-894-17

Qy   663   ACGATTGCCAACACATACTTCT   684
              ||||||||||||||||||||||
Db   22   ACGATTGCCAACACATACTTCT   1

Query Match   2.8%;   Score 22;   DB 33;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 1.7;
Matches   22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 11
PCT-US99-29593-2/c
Sequence 2, Application PC/TUS9929593
GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.

; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-2

Query Match   2.6%; Score 20; DB 1; Length 20;
Best Local Similarity   100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GAGTGAGCATTCTCAGCACA 20
        ||||||||||||||||||||
Db   20 GAGTGAGCATTCTCAGCACA 1

RESULT 12
PCT-US99-29593-3/c
; Sequence 3, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-3

Query Match   2.6%; Score 20; DB 1; Length 20;
Best Local Similarity   100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   19 CATTGCCTCAACAGCTTCAA 38
        ||||||||||||||||||||
Db   20 CATTGCCTCAACAGCTTCAA 1

RESULT 13
PCT-US99-29593-4/c
; Sequence 4, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432

; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-4

Query Match   2.6%; Score 20; DB 1; Length 20;
Best Local Similarity   100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   39 GGTGACCAGCTCAAGACTT 58
        ||||||||||||||||||||
Db   20 GGTGACCAGCTCAAGACTT 1

RESULT 14
PCT-US99-29593-5/c
; Sequence 5, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-5

Query Match   2.6%; Score 20; DB 1; Length 20;
Best Local Similarity   100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   66 CACCAGGCAGAAGATGACAG 85
        ||||||||||||||||||||
Db   20 CACCAGGCAGAAGATGACAG 1

RESULT 15
PCT-US99-29593-6/c
; Sequence 6, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568

```
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
; PCT-US99-29593-6

Query Match           2.6%;  Score 20;  DB 1;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 21;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       91 GAATTTGGATATATTTACAG 110
            ||||||||||||||||||||
Db       20 GAATTTGGATATATTTACAG 1
```

Search completed: March 14, 2003, 10:27:59
Job time : 1151.99 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 04:47:29 ; Search time 213.449 Seconds
                      (without alignments)
                      8302.956 Million cell updates/sec

Title: US-09-869-894-1
Perfect score: 780
Sequence: 1 gagtgagcattctcagcaca.........aattgtatgtattttctct 780

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4666902 seqs, 1136064160 residues
Word size : 0

Total number of hits satisfying chosen parameters: 7027196

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	6.4	50	8	US-10-325-899-2596	Sequence 2596, Ap
2	50	6.4	50	8	US-10-325-899-3838	Sequence 3838, Ap
3	22	2.8	25	8	US-10-427-836-533438	Sequence 533438,
4	21	2.7	21	8	US-10-310-188-73875	Sequence 73875, A
5	19	2.4	19	8	US-10-310-188-85737	Sequence 85737, A
6	19	2.4	25	8	US-60-427-836-6872	Sequence 6872, Ap
7	18	2.3	25	9	US-60-427-836-59598	Sequence 59598, A
8	17	2.2	25	9	US-60-427-808-360861	Sequence 360861,
9	17	2.2	24	8	US-60-427-808-757664	Sequence 757664,
10	16	2.1	25	9	US-10-303-778-10504	Sequence 10504, A
11	16	2.1	25	8	US-10-355-577-67556	Sequence 67556, A
12	16	2.1	25	8	US-10-355-577-149144	Sequence 149144,
13	16	2.1	25	8	US-10-355-577-249093	Sequence 249093,
14	16	2.1	25	8	US-10-355-577-317546	Sequence 317546,
15	16	2.1	25	8	US-10-355-577-487471	Sequence 487471,
16	16	2.1	25	8	US-10-355-577-535019	Sequence 535019,
17	16	2.1	25	8	US-60-427-808-272157	Sequence 272157,
18	16	2.1	25	9	US-60-427-808-415756	Sequence 415756,
19	16	2.1	25	9	US-60-427-808-595802	Sequence 595802,
20	16	2.1	25	9	US-60-427-808-730126	Sequence 730126,
21	16	2.1	25	9	US-60-427-808-875365	Sequence 875365,
22	16	2.1	25	9	US-60-427-836-238638	Sequence 238638,
23	16	2.1	25	9	US-60-427-836-242560	Sequence 242560,
24	16	2.1	25	9	US-60-427-836-500999	Sequence 500999,
25	15	1.9	22	1	PCT-IL02-00722-5	Sequence 5, Appli
26	15	1.9	25	8	US-10-098-263B-55291	Sequence 55291, A
27	15	1.9	25	8	US-10-098-263B-92039	Sequence 92039, A
28	15	1.9	25	8	US-10-355-577-2912	Sequence 2912, Ap
29	15	1.9	25	8	US-10-355-577-9159	Sequence 9159, Ap
30	15	1.9	25	8	US-10-355-577-51855	Sequence 51855, A
31	15	1.9	25	8	US-10-355-577-377737	Sequence 377737,
32	15	1.9	25	8	US-10-355-577-461582	Sequence 461582,
33	15	1.9	25	8	US-10-355-577-686435	Sequence 686435,
34	15	1.9	25	8	US-10-355-577-719610	Sequence 719610,
35	15	1.9	25	8	US-10-355-577-740801	Sequence 740801,
36	15	1.9	25	8	US-10-355-577-842893	Sequence 842893,
37	15	1.9	25	8	US-10-355-577-934308	Sequence 934308,
38	15	1.9	25	8	US-60-417-190-381	Sequence 381, App
39	15	1.9	25	8	US-60-417-190-382	Sequence 382, App
40	15	1.9	25	9	US-60-417-190-3459	Sequence 3459, Ap
41	15	1.9	25	9	US-60-417-190-3460	Sequence 3460, Ap
42	15	1.9	25	9	US-60-427-808-172458	Sequence 172458,
43	15	1.9	25	9	US-60-427-808-188567	Sequence 188567,
44	15	1.9	25	9	US-60-427-808-333996	Sequence 333996,
45	15	1.9	25	9	US-60-427-808-398418	Sequence 398418,

ALIGNMENTS

RESULT 1
US-10-325-899-2596
; Sequence 2596, Application US/10325899
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPL
; FILE REFERENCE: 50661200000122
; CURRENT APPLICATION NUMBER: US/10/325,899
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2596
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-899-2596

Query Match   6.4%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  703 TTGATGATGTAACTTGACCTTCCACAGTTTATGGAAATTTTGTCCCCATGT 752
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TTGATGATGTAACTTGACCTTCCACAGTTTATGGAAATTTTGTCCCCATGT 50
```

RESULT 2
US-10-325-899-3838
; Sequence 3838, Application US/10325899
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPL
; FILE REFERENCE: 50661200000122

```
; CURRENT APPLICATION NUMBER: US/10,325,899
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 3838
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-899-3838

Query Match             6.4%;  Score 50;  DB 8;  Length 50;
Best Local Similarity   100.0%;  Pred. No. 1.2e-16;
Matches   50;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    703 TTGATGAATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTGATGAATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50


RESULT 3
US-60-427-836-533438
Sequence 533438, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-533438

Query Match             2.8%;  Score 22;  DB 9;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 0.23;
Matches   22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    519 GTTTGAACCTAAATCTGGCTGG 540
          ||||||||||||||||||||||
Db      1 GTTTGAACCTAAATCTGGCTGG 22


RESULT 4
US-10-310-188-73875/c
Sequence 73875, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 73875
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-73875

Query Match             2.7%;  Score 21;  DB 8;  Length 21;
Best Local Similarity   100.0%;  Pred. No. 0.8;
Matches   21;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Qy    733 TGGAAATTTTGTCCCCATGTA 753
          |||||||||||||||||||||
Db     21 TGGAAATTTTGTCCCCATGTA 1


RESULT 5
US-10-310-188-85737/c
Sequence 85737, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY (
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 85737
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85737

Query Match             2.4%;  Score 19;  DB 8;  Length 19;
Best Local Similarity   100.0%;  Pred. No. 9.8;
Matches   19;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     56 CTTTGCTCTCCACCAGGCA 74
          |||||||||||||||||||
Db     19 CTTTGCTCTCCACCAGGCA 1


RESULT 6
US-60-427-836-6872
Sequence 6872, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-6872

Query Match             2.4%;  Score 19;  DB 9;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 9.9;
Matches   19;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    173 AAACGTCCAGAGTGCTACA 191
          |||||||||||||||||||
Db      1 AAACGTCCAGAGTGCTACA 19


RESULT 7
US-60-427-836-59598
Sequence 59598, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
```

```
US-60-427-836-59598

  Query Match             2.3%;  Score 18;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        165 TCCAAGCAAAACGTCCAG 182
              ||||||||||||||||||
Db          8 TCCAAGCAAAACGTCCAG 25

RESULT 8
US-60-427-808-360861
; Sequence 360861, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 360861
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-360861

  Query Match             2.2%;  Score 17;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        119 AGGACTACTGCAGTGC 135
              |||||||||||||||
Db          3 AGGACTACTGCAGTGC 19

RESULT 9
US-60-427-808-757664/c
; Sequence 757664, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 757664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-757664

  Query Match             2.2%;  Score 17;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        210 CCAAAAAGAAGTGGAAA 226
              ||||||||||||||||
Db         20 CCAAAAAGAAGTGGAAA 4

RESULT 10
US-10-303-778-10504/c
; Sequence 10504, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
```

```
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10504
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Infectious hypodermal and hematopoietic necrosis virus
US-10-303-778-10504

  Query Match             2.1%;  Score 16;  DB 8;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   16;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        304 GAAAAGGAGTTTGAAG 319
              ||||||||||||||||
Db         19 GAAAAGGAGTTTGAAG 4

RESULT 11
US-10-355-577-67556/c
; Sequence 67556, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-67556

  Query Match             2.1%;  Score 16;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   16;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        551 TAGAAGTTACAGGAAA 566
              ||||||||||||||||
Db         23 TAGAAGTTACAGGAAA 8

RESULT 12
US-10-355-577-149144
; Sequence 149144, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-149144

  Query Match             2.1%;  Score 16;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   16;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        380 AGAAACTTCTACGACA 395
              ||||||||||||||||
Db          1 AGAAACTTCTACGACA 16

RESULT 13
US-10-355-577-249093
; Sequence 249093, Application US/10355577
; GENERAL INFORMATION:
```

```
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;  SEQ ID NO 249093
;  LENGTH: 25
;  TYPE: DNA
;  ORGANISM: Homo sapien
US-10-355-577-249093

Qy        64 TCCACCAGGCAGAAGA 79
              ||||||||||||||||
Db         4 TCCACCAGGCAGAAGA 19

Query Match          2.1%;  Score 16;  DB 8;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
Matches  16;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

US-10-355-577-317546

RESULT 14
US-10-355-577-317546
;  Sequence 317546, Application US/10355577
;  GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;  SEQ ID NO 317546
;  LENGTH: 25
;  TYPE: DNA
;  ORGANISM: Homo sapien
US-10-355-577-317546

Qy       252 TGTTAATGTTGTGTCC 267
              ||||||||||||||||
Db         5 TGTTAATGTTGTGTCC 20

Query Match          2.1%;  Score 16;  DB 8;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
Matches  16;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

US-10-355-577-487471

RESULT 15
US-10-355-577-487471/c
;  Sequence 487471, Application US/10355577
;  GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;  SEQ ID NO 487471
;  LENGTH: 25
;  TYPE: DNA
;  ORGANISM: Homo sapien
US-10-355-577-487471

Qy       606 ACCAGAAAGGACACTC 621
              ||||||||||||||||
Db        21 ACCAGAAAGGACACTC 6

Query Match          2.1%;  Score 16;  DB 8;  Length 25;
Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
Matches  16;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:08:08 ;
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Search time 6850.7 Seconds
(without alignments)
16712.222 Million cell updates/sec

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccagtaaggagtcgggtc..........aaatctttattcaaataaa 3934

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 1455140878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_vrt:*
16: gb_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_pr:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_un:*
31: em_htg_hum:*
32: em_htg_inv:*
33: em_htg_other:*
34: em_htg_mus:*
35: em_htg_pln:*
36: em_htg_rod:*
37: em_htg_mam:*
38: em_htg_vrt:*
39: em_sy:*
40: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
C	1	21	0.5	21	6	I86713	I86713 Sequence 1
C	2	20	0.5	20	6	AR095066	AR095066 Sequence
C	3	20	0.5	20	6	AR095067	AR095067 Sequence
C	4	20	0.5	20	6	AR095068	AR095068 Sequence
C	5	20	0.5	20	6	AR095069	AR095069 Sequence
C	6	20	0.5	20	6	AR095070	AR095070 Sequence
C	7	20	0.5	20	6	AR095071	AR095071 Sequence
C	8	20	0.5	20	6	AR095072	AR095072 Sequence
C	9	20	0.5	20	6	AR095073	AR095073 Sequence
C	10	20	0.5	20	6	AR095074	AR095074 Sequence
C	11	20	0.5	20	6	AR095075	AR095075 Sequence
C	12	20	0.5	20	6	AR095076	AR095076 Sequence
C	13	20	0.5	20	6	AR095077	AR095077 Sequence
C	14	20	0.5	20	6	AR095078	AR095078 Sequence
C	15	20	0.5	20	6	AR095079	AR095079 Sequence
C	16	20	0.5	20	6	AR095080	AR095080 Sequence
C	17	20	0.5	20	6	AR095081	AR095081 Sequence
C	18	20	0.5	20	6	AR095082	AR095082 Sequence
C	19	20	0.5	20	6	AR095083	AR095083 Sequence
C	20	20	0.5	20	6	AR095084	AR095084 Sequence
C	21	20	0.5	20	6	AR095085	AR095085 Sequence
C	22	20	0.5	20	6	I86715	I86715 Sequence 3
C	23	20	0.5	26	6	I86729	I86729 Sequence 17
C	24	18	0.5	33	6	I15222	I15222 Sequence 1
C	25	18	0.5	38	6	A67648	A67648 Sequence 68
C	26	18	0.5	38	6	AR089924	AR089924 Sequence
C	27	18	0.5	44	6	AX236881	AX236881 Sequence
C	28	18	0.5	44	6	AX239777	AX239777 Sequence
C	29	17	0.4	20	6	AX488424	AX488424 Sequence
C	30	17	0.4	21	6	A20477	A20477 Oligonucleo
C	31	17	0.4	24	6	AX250150	AX250150 Sequence
C	32	17	0.4	24	6	I86728	I86728 Sequence 16
C	33	17	0.4	45	6	AX009974	AX009974 Sequence
C	34	17	0.4	45	6	AX236883	AX236883 Sequence
C	35	17	0.4	45	6	AX236902	AX236902 Sequence
C	36	17	0.4	45	6	AX239779	AX239779 Sequence
C	37	17	0.4	45	6	AX239796	AX239796 Sequence
C	38	17	0.4	47	6	AX136052	AX136052 Sequence
C	39	17	0.4	50	6	I08559	I08559 Sequence 1
C	40	16	0.4	19	6	AR165304	AR165304 Sequence
C	41	16	0.4	20	6	AX488272	AX488272 Sequence
C	42	16	0.4	21	6	AR084547	AR084547 Sequence
C	43	16	0.4	21	6	AR084559	AR084559 Sequence
C	44	16	0.4	21	6	AR084561	AR084561 Sequence
C	45	16	0.4	21	6	AR084584	AR084584 Sequence

ALIGNMENTS

RESULT 1
I86713/c
LOCUS   I86713   21 bp   DNA   linear   PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5702897.
ACCESSION   I86713
VERSION   I86713.1 GI:3206431
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 21)
  AUTHORS   Reed,J.C. and Sato,T.
  TITLE   Interaction of proteins involved in a cell death pathway
  JOURNAL   Patent: US 5702897-A 1 30-DEC-1997;
FEATURES   Location/Qualifiers

q

```
                source  1..21
                        /organism="unknown"
BASE COUNT        4 a        8 c        2 g        7 t
ORIGIN
Qy   1235 GCAAGTGCCAAGAGGATTATG 1255
          ||||||||||||||||||||||
Db     21 GCAAGTGCCAAGAGGATTATG 1

Query Match             100.0%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 10;
  Matches 21;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 2
AR095066/c
LOCUS       AR095066                   20 bp    DNA        linear   PAT 08-SEP-2000
DEFINITION  Sequence 19 from patent US 6001992.
ACCESSION   AR095066
VERSION     AR095066.1  GI:10022583
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 19 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT        5 a        8 c        4 g        3 t
ORIGIN
Qy     50 GGCGACTGGCAATGTTTGGC 69
          ||||||||||||||||||||
Db     20 GGCGACTGGCAATGTTTGGC 1

Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 39;
  Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 3
AR095067/c
LOCUS       AR095067                   20 bp    DNA        linear   PAT 08-SEP-2000
DEFINITION  Sequence 20 from patent US 6001992.
ACCESSION   AR095067
VERSION     AR095067.1  GI:10022585
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 20 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT        5 a        9 c        4 g        2 t
ORIGIN
Qy    152 CGGGGAGGGGGGACTTTTGGCT 171
          ||||||||||||||||||||||
Db     20 CGGGGAGGGGGGACTTTTGGCT 1

Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 39;
  Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 4
```

```
AR095068/c
LOCUS       AR095068                   20 bp    DNA        linear   PAT 08-SEP-2000
DEFINITION  Sequence 21 from patent US 6001992.
ACCESSION   AR095068
VERSION     AR095068.1  GI:10022587
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 21 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT        2 a       10 c        3 g        5 t
ORIGIN
Qy    431 AGGAGCTGGACGGGGTACGAG 450
          |||||||||||||||||||||
Db     20 AGGAGCTGGACGGGGTACGAG 1

Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 39;
  Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 5
AR095069/c
LOCUS       AR095069                   20 bp    DNA        linear   PAT 08-SEP-2000
DEFINITION  Sequence 22 from patent US 6001992.
ACCESSION   AR095069
VERSION     AR095069.1  GI:10022589
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 22 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT        4 a        6 c        3 g        7 t
ORIGIN
Qy    501 CGGGGAATCTGGTAATAACA 520
          ||||||||||||||||||||
Db     20 CGGGGAATCTGGTAATAACA 1

Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 39;
  Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 6
AR095070/c
LOCUS       AR095070                   20 bp    DNA        linear   PAT 08-SEP-2000
DEFINITION  Sequence 23 from patent US 6001992.
ACCESSION   AR095070
VERSION     AR095070.1  GI:10022591
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 23 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
```

```
BASE COUNT      9 a      7 c      4 g      0 t
ORIGIN

Qy        636 CGCCAAGGACACAAAGCCAA 655
              ||||||||||||||||||||
Db         20 CGCCAAGGACACAAAGCCAA 1


RESULT 7
AR095071/c
LOCUS       AR095071                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 24 from patent US 6001992.
ACCESSION   AR095071
VERSION     AR095071.1  GI:10022593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 24 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT      3 a      4 c      8 g      5 t
ORIGIN

Query Match             0.5%;  Score 20;  DB 6;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 39;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        842 GGGGCAGGAATTGTGACTCTC 861
              ||||||||||||||||||||
Db         20 GGGGCAGGAATTGTGACTCTC 1


RESULT 8
AR095072/c
LOCUS       AR095072                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 25 from patent US 6001992.
ACCESSION   AR095072
VERSION     AR095072.1  GI:10022595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 25 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT      3 a      3 c      7 g      7 t
ORIGIN

Query Match             0.5%;  Score 20;  DB 6;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 39;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1045 AGGAATGTGCTGCTGGCTTT 1064
              ||||||||||||||||||||
Db         20 AGGAATGTGCTGCTGGCTTT 1


RESULT 9
AR095073/c
LOCUS       AR095073                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 26 from patent US 6001992.
ACCESSION   AR095073
VERSION     AR095073.1  GI:10022597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 26 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT      9 a      3 c      7 g      1 t
ORIGIN

Query Match             0.5%;  Score 20;  DB 6;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 39;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1230 GAAAAGCAAGTGGGCAAGAGG 1249
              ||||||||||||||||||||
Db         20 GAAAACCAAGTGGGCAAGAGG 1


RESULT 10
AR095074/c
LOCUS       AR095074                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 27 from patent US 6001992.
ACCESSION   AR095074
VERSION     AR095074.1  GI:10022599
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 27 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
BASE COUNT      6 a      4 c      6 g      4 t
ORIGIN

Query Match             0.5%;  Score 20;  DB 6;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 39;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1519 AAGAATGCCAGTGACCTGTG 1538
              ||||||||||||||||||||
Db         20 AAGAATGCCAGTGACCTGTG 1


RESULT 11
AR095075/c
LOCUS       AR095075                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 28 from patent US 6001992.
ACCESSION   AR095075
VERSION     AR095075.1  GI:10022601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 28 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
```

```
BASE COUNT        9 a    5 c    4 g    2 t
ORIGIN

Query Match      Best Local Similarity  100.0%;      Score 20;  DB 6;  Length 20;
                 Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
                                                    Pred. No. 39;

Qy  1676  GGCTTGGTTCCATGAATTCTT  1695
          ||||||||||||||||||||
Db    20  GGCTTGGTTCCATGAATTCTT  1

RESULT 12
LOCUS       AR095076/c              20 bp    DNA    linear    PAT 08-SEP-2000
DEFINITION  Sequence 29 from patent US 6001992.
ACCESSION   AR095076
VERSION     AR095076.1  GI:10022603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 29 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
                     1..20

BASE COUNT        4 a    7 c    2 g    7 t
ORIGIN

Query Match      Best Local Similarity  100.0%;      Score 20;  DB 6;  Length 20;
                 Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
                                                    Pred. No. 39;

Qy  2091  TGAAAACCTGGGATTGAGAG  2110
          ||||||||||||||||||||
Db    20  TGAAAACCTGGGATTGAGAG  1

RESULT 13
LOCUS       AR095077/c              20 bp    DNA    linear    PAT 08-SEP-2000
DEFINITION  Sequence 30 from patent US 6001992.
ACCESSION   AR095077
VERSION     AR095077.1  GI:10022605
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 30 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
                     1..20

BASE COUNT        8 a    3 c    6 g    3 t
ORIGIN

Query Match      Best Local Similarity  100.0%;      Score 20;  DB 6;  Length 20;
                 Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
                                                    Pred. No. 39;

Qy  2231  TGAGTTCCTTCCATTTGACC  2250
          ||||||||||||||||||||
Db    20  TGAGTTCCTTCCATTTGACC  1

RESULT 14
LOCUS       AR095078/c              20 bp    DNA    linear    PAT 08-SEP-2000
DEFINITION  Sequence 31 from patent US 6001992.
ACCESSION   AR095078
VERSION     AR095078.1  GI:10022607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 31 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
                     1..20

BASE COUNT        5 a    9 c    1 g    5 t
ORIGIN

Query Match      Best Local Similarity  100.0%;      Score 20;  DB 6;  Length 20;
                 Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
                                                    Pred. No. 39;

Qy  2366  GGTGGATGGAGAGACATTTG  2385
          ||||||||||||||||||||
Db    20  GGTGGATGGAGAGACATTTG  1

RESULT 15
LOCUS       AR095079/c              20 bp    DNA    linear    PAT 08-SEP-2000
DEFINITION  Sequence 32 from patent US 6001992.
ACCESSION   AR095079
VERSION     AR095079.1  GI:10022609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of novel anti-apoptotic bcl-2-related proteins
  JOURNAL   Patent: US 6001992-A 32 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="unknown"
                     1..20

BASE COUNT        9 a    5 c    3 g    3 t
ORIGIN

Query Match      Best Local Similarity  100.0%;      Score 20;  DB 6;  Length 20;
                 Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
                                                    Pred. No. 39;

Qy  2564  GCATTGGCCATCTTTGGATTT  2583
          ||||||||||||||||||||
Db    20  GCATTGGCCATCTTTGGATTT  1
```

Search completed: March 14, 2003, 07:13:19
Job time : 6854.2 secs

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 03:41:43 ; Search time 575.829 Seconds

       GenCore version 5.1.4_p5_4578
       Copyright (c) 1993 - 2003 Compugen Ltd.

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccagtaaggagtcggggtc........aaatctttattcaaataaa 3934

Scoring table: OLIGO_NUC
       Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_101002:*

```
1:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000lA.DAT:*
23:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001lA.DAT:*
24:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	0.8	30	22	AAD06442	Human Mcl-1 DNA ex
2	21	0.5	21	16	AAT03164	Human Mcl-1 gene f
3	21	0.5	21	20	AAX26538	PCR primer P12. S
4	21	0.5	21	22	AAX26539	PCR primer P13. S
5	21	0.5	21	22	AAD06439	Human Mcl-1 cDNA a
6	21	0.5	21	22	AAD06441	Human Mcl-1 cDNA a
7	20	0.5	21	16	AAT03166	Human Mcl-1 gene r
8	20	0.5	20	18	AAZ39083	Human mcl-1 anti-a
9	20	0.5	20	21	AAZ39084	Human mcl-1 anti-a

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AAD06442/c
ID   AAD06442 standard; DNA; 30 BP.
XX
AC   AAD06442;
XX
DT   10-AUG-2001 (first entry)
XX
DE   Human Mcl-1 DNA extending PCR primer, #105C.
XX
KW   Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant;
KW   neuronal cell; tumour cell; apoptosis; therapy; cancer; psoriasis;
KW   diabetic retinopathy; corneal graft neovascularisation;
KW   neovascular glaucoma; epithelial condition; autoimmune disease;
KW   rheumatoid arthritis; systemic lupus erythematosus;
KW   neurodegenerative disease; PCR primer; ss.
OS   Homo sapiens.
XX
PN   WO200136594-A1.
XX
PD   25-MAY-2001.
XX
PF   14-JAN-2000; 2000WO-US00969.
XX
PR   16-NOV-1999; 99US-0166113.
XX
PA   (DART-) DARTMOUTH COLLEGE.
XX
PI   Craig RW, Bingle CD, Whyte M;
XX
DR   WPI; 2001-343812/36.

c	10	20	21	AAZ39085	Human mcl-1 anti-a
c	11	20	21	AAZ39086	Human mcl-1 anti-a
c	12	20	21	AAZ39087	Human mcl-1 anti-a
c	13	20	21	AAZ39090	Human mcl-1 anti-a
c	14	20	21	AAZ39091	Human mcl-1 anti-a
c	15	20	21	AAZ39092	Human mcl-1 anti-a
c	16	20	21	AAZ39093	Human mcl-1 anti-a
c	17	20	21	AAZ39094	Human mcl-1 anti-a
c	18	20	21	AAZ39095	Human mcl-1 anti-a
c	19	20	21	AAZ39096	Human mcl-1 anti-a
c	20	20	21	AAZ39097	Human mcl-1 anti-a
c	21	20	21	AAZ39098	Human mcl-1 anti-a
c	22	20	21	AAZ39099	Human mcl-1 anti-a
c	23	20	21	AAZ39100	Human mcl-1 anti-a
c	24	20	21	AAZ39101	Human mcl-1 anti-a
c	25	20	21	AAZ39102	Human mcl-1 anti-a
c	26	20	21	AAZ39103	Human mcl-1 anti-a
c	27	20	21	AAZ39104	Human mcl-1 anti-a
c	28	20	22	AAH76277	Human myeloid leuk
c	29	20	22	AAH76278	Human myeloid leuk
c	30	20	22	AAD06437	Human Mcl-1 cDNA a
c	31	20	22	AAD06438	Human Mcl-1 cDNA a
c	32	20	22	AAD06440	Human Mcl-1 CDNA a
c	33	20	19	AAV39021	GnT-IV cDNA contai
c	34	20	19	AAQ41910	erb B2/neu promote
c	35	18	21	AAC63775	Guanosine rich oli
c	36	18	21	AAC63576	Guanosine rich oli
c	37	18	19	AAV16068	PCR primer used to
c	38	18	21	AAA05350	PCR primer SrYMn18
c	39	18	21	AAZ43365	Murine Srv gene PC
c	40	18	14	AAQ41909	erb B2/neu promote
c	41	18	14	AAQ55568	Sequence of synthe
c	42	18	15	AAQ55567	Sequence of synthe
c	43	18	15	AAO67228	Triple helix-form1
c	44	18	22	AAS44314	Neisseria meningit
c	45	18	22	AAD17079	N. meningitidis fu

```
XX
PT   Novel Mcl-1 gene regulatory elements, useful for modulating expression
PT   of Mcl-1 polypeptide or its variant which regulate apoptosis in
PT   neuronal or tumor cells -
XX
PS   Example 2; Page 76; 125pp; English.
XX
CC   The present invention relates to Mcl-1 gene regulatory elements and the
CC   variant Mcl-1s/DeltaTM. The anti-apoptotic Mcl-1 protein is encoded by
CC   exons 1, 2 and 3. The pro-apoptotic Mcl-1s/DeltaTM variant encoded by
CC   exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1
CC   gene regulatory element is useful for modulating the Mcl-1 gene
CC   expression in a cell e.g., neuronal cell or tumour cell, such that
CC   apoptosis of the cell is induced or cell viability is increased. The
CC   Mcl-1 and its regulatory elements are used for treating pathological
CC   conditions which include cancer, diabetic retinopathy, corneal graft
CC   neovascularisation and neovascular glaucoma, epithelial conditions such
CC   as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic
CC   lupus erythematosus, and neurodegenerative diseases. The present sequence
CC   is a PCR primer #105c, used for the extension reaction of the human
CC   Mcl-1 DNA.
XX
SQ   Sequence 30 BP; 7 A; 9 C; 8 G; 6 T; 0 other;

Query Match
Best Local Similarity   100.0%;  Score 30;  DB 22;  Length 30;
Matches  30;  Conservative  0;  Pred. No. 0.00072;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   83 CGGTAATCGGACTCAACCTCTACTGTGGGG 112
         ||||||||||||||||||||||||||||||
Db   30 CGGTAATCGGACTCAACCTCTACTGTGGGG 1


RESULT 2
AAT03164/c;

ID   AAT03164 standard; DNA; 21 BP.
AC   AAT03164;
XX
DT   05-JUN-1996  (first entry)
XX
DE   Human Mcl-1 gene first strand primer.
XX
KW   Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel;
KW   detection; ss.
XX
OS   Synthetic.
XX
PN   WO9528497-A1.
XX
PD   26-OCT-1995.
XX
PF   12-APR-1995;  95WO-US04600.
XX
PR   13-APR-1994;  94US-0226876.
XX
PA   (LJOL-) LA JOLLA CANCER RES FOUND.
PI   Reed JC,  Sato T;
XX
DR   WPI; 1995-373811/48.
XX
PT   Detection of novel proteins involved in apoptosis
PT   with proteins involved in apoptosis - by interaction
XX
PS   Example 1; Page 22; 62pp; English.
XX
CC   AAT03164-T03366 are primers used for the amplification of the human
CC   Mcl-1 gene. The Mcl-1 protein is a Bcl-2 related protein, the Mcl-1
CC   protein was expressed and used to investigate the interactions of
CC   Mcl-1 with other proteins known to be involved in apoptosis
CC   (excluding the Bax protein). Proteins detected using this method can
CC   act as upstream activators or downstream effectors of a cellular
CC   protein such as Bax which induces apoptosis levels. If the protein is a
CC   Bcl-2 related protein apoptosis levels are decreased due to the
CC   protein binding to and inactivating Bax.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 other;

Query Match
Best Local Similarity   100.0%;  Score 21;  DB 16;  Length 21;
Matches  21;  Conservative  0;  Pred. No. 17;  Mismatches  0;  Indels  0;  Gaps  0;

Qy 1235 GCAAGTGGCAAGAGGATTATG 1255
        |||||||||||||||||||||
Db   21 GCAAGTGGCAAGAGGATTATG 1


RESULT 3
AAX26538

ID   AAX26538 standard; DNA; 21 BP.
AC   AAX26538;
XX
DT   27-MAY-1999  (first entry)
XX
DE   PCR primer P12.
XX
KW   DNA amplification; nucleotide analogue; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9909213-A1.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1997;  97JP-0231885.
PR   21-OCT-1997;  97JP-0305016.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
PI   Hino F,  Kato I,  Mukai H,  Yamamoto J;
XX
DR   WPI; 1999-181059/15.
XX
PT   Simple and accurate method for DNA amplification - uses
PT   amplification in the presence of nucleotide analogues together with
PT   a compound which lowers the Tm of double-stranded nucleic acids
XX
PS   Example 6; Page 31; 36pp; Japanese.
XX
CC   PCR primers AAX26538-39 were used to exemplify the invention. The
CC   specification describes methods for DNA amplification, wherein a
CC   template DNA containing nucleotide analogues is amplified in
CC   the presence of nucleotide analogues and a substance which lowers
CC   the Tm value of double-stranded nucleic acids. Suitable nucleotide
CC   analogues are 7-deaza-dGTP, 7-deaza-dATP, dITP and hydroxymethyl-dUTP.
CC   Suitable Tm value-lowering substances are formamide, dimethyl sulphoxide
CC   and trimethylglycine. The methods improve the amplification of DNA.
CC   Also, DNA fragments which originated as RNA can be amplified without
CC   purifying the RNAs in sample.
XX
SQ   Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 other;

Query Match
Best Local Similarity   100.0%;  Score 21;  DB 20;  Length 21;
Matches  21;  Conservative  0;  Pred. No. 17;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  586 CGGCAGTCGCTGGAGATTATC 606
        |||||||||||||||||||||
Db    1 CGGCAGTCGCTGGAGATTATC 21


RESULT 4
```

ID   AAX26539 standard; DNA; 21 BP.
XX
AC   AAX26539;
XX
DT   27-MAY-1999 (first entry)
XX
DE   PCR primer P13.
XX
KW   DNA amplification; nucleotide analogue; PCR primer; ss.
OS   Synthetic.
XX
PN   WO9909213-A1.
XX
PD   25-FEB-1999.
XX
PF   10-AUG-1998;   98WO-JP03566.
XX
PR   21-OCT-1997;   97JP-0305016.
PR   14-AUG-1997;   97JP-0231885.
XX
PA   (TAKI) TAKARA SHUZO CO LTD.
XX
PI   Hino F, Kato I, Mukai H, Yamamoto J;
XX
DR   WPI; 1999-181059/15.
XX
PT   Simple and accurate method for DNA amplification - uses
PT   amplification in the presence of nucleotide analogues together with
PT   a compound which lowers the Tm of double-stranded nucleic acids
XX
PS   Example 6; Page 31; 36pp; Japanese.
XX
CC   PCR primers AAX26538-39 were used to exemplify the invention. The
CC   specification describes methods for DNA amplification, wherein a
CC   template DNA containing nucleotide analogues is amplified in
CC   the presence of nucleotide analogues and a substance which lowers
CC   the Tm value of double-stranded nucleic acids. Suitable nucleotide
CC   analogues are 7-deaza-dGTP, 7-deaza-dATP, dITP and hydroxymethyl-dUTP.
CC   Suitable Tm value-lowering substances are formamide, dimethyl sulphoxide
CC   and trimethylglycine. The methods improve the amplification of DNA.
CC   Also, DNA fragments which originated as RNA can be amplified without
CC   purifying the RNAs in sample.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 other;

Query Match   0.5%;   Score 21;   DB 20;   Length 21;
Best Local Similarity   100.0%;   Pred. No. 17;
Matches   21;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1014 CTTCCAHGTAGAGGACCTAGA 1034
               |||||||||||||||||||||
Db   21 CTTCCAHGTAGAGGACCTAGA 1

RESULT 5
ID   AAD06439
ID   AAD06439 standard; DNA; 21 BP.
XX
AC   AAD06439;
XX
DT   10-AUG-2001 (first entry)
XX
DE   Human Mcl-1 cDNA amplifying RT-PCR primer, Mcl-1-F5.
XX
KW   Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant;
KW   neuronal cell; tumour cell; apoptosis; therapy; cancer; psoriasis;
KW   diabetic retinopathy; corneal graft neovascularisation;
KW   neovascular glaucoma; epithelial condition; autoimmune disease;
KW   rheumatoid arthritis; systemic lupus erythematosus;
KW   neurodegenerative disease; PCR primer; ss.

OS   Homo sapiens.
XX
PN   WO200136594-A1.
XX
PD   25-MAY-2001.
XX
PF   14-JAN-2000; 2000WO-US00969.
XX
PR   16-NOV-1999;   99US-0166113.
XX
PA   (DART-) DARTMOUTH COLLEGE.
XX
PI   Craig RW, Bingle CD, Whyte M;
XX
DR   WPI; 2001-343812/36.
XX
PT   Novel Mcl-1 gene regulatory elements, useful for modulating expression
PT   of Mcl-1 polypeptide or its variant which regulate apoptosis in
PT   neuronal or tumor cells -
XX
PS   Example 2; Page 75; 125pp; English.
XX
CC   The present invention relates to Mcl-1 gene regulatory elements and the
CC   variant Mcl-1s/deltaTM. The anti-apoptotic Mcl-1 protein is encoded by
CC   exons 1, 2 and 3. The pro-apoptotic Mcl-1s/DeltaTM variant encoded by
CC   exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1
CC   gene regulatory element is useful for modulating the Mcl-1 gene
CC   expression in a cell e.g., neuronal cell or tumour cell, such that
CC   apoptosis of the cell is induced or cell viability is increased. The
CC   Mcl-1 and its regulatory elements are used for treating pathological
CC   conditions which include cancer, diabetic retinopathy, corneal graft
CC   neovascularisation and neovascular glaucoma, epithelial conditions such
CC   as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic
CC   lupus erythematosus, and neurodegenerative diseases. The present sequence
CC   is a RT-PCR primer Mcl-1-F5, used for the amplification of the human
CC   Mcl-1 cDNA.
XX
SQ   Sequence 21 BP; 3 A; 5 C; 8 G; 5 T; 0 other;

Query Match   0.5%;   Score 21;   DB 22;   Length 21;
Best Local Similarity   100.0%;   Pred. No. 17;
Matches   21;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   5 GTAAGGAGTCGGGGTCTTCCC 25
               |||||||||||||||||||||
Db   1 GTAAGGAGTCGGGGTCTTCCC 21

RESULT 6
ID   AAD06441/c
ID   AAD06441 standard; DNA; 21 BP.
XX
AC   AAD06441;
XX
DT   10-AUG-2001 (first entry)
XX
DE   Human Mcl-1 cDNA amplifying RT-PCR primer, Mcl-1-R7.
XX
KW   Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant;
KW   neuronal cell; tumour cell; apoptosis; therapy; cancer; psoriasis;
KW   diabetic retinopathy; corneal graft neovascularisation;
KW   neovascular glaucoma; epithelial condition; autoimmune disease;
KW   rheumatoid arthritis; systemic lupus erythematosus;
KW   neurodegenerative disease; PCR primer; ss.

OS   Homo sapiens.
XX
PN   WO200136594-A1.
XX
PD   25-MAY-2001.
XX
PF   14-JAN-2000; 2000WO-US00969.

```
PR   16-NOV-1999;   99US-0166113.
PA   (DART-) DARTMOUTH COLLEGE.
XX
PI   Craig RW, Bingle CD, Whyte M;
XX
DR   WPI; 2001-343812/36.
XX
PT   Novel Mcl-1 gene regulatory elements, useful for modulating expression
     of Mcl-1 polypeptide or its variant which regulate apoptosis in
     neuronal or tumor cells -
XX
PS   Example 2; Page 75; 125pp; English.
XX
CC   The present invention relates to Mcl-1 gene regulatory elements and the
CC   variant Mcl-1s/deltaTM. The anti-apoptotic Mcl-1 protein is encoded by
CC   exons 1, 2 and 3. The pro-apoptotic Mcl-1s/DeltaTM variant encoded by
CC   exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1
CC   gene regulatory element is useful for modulating the Mcl-1 gene
CC   expression in a cell e.g. neuronal cell or tumour cell, such that
CC   apoptosis of the cell is induced or cell viability is increased. The
CC   Mcl-1 and its regulatory elements are used for treating pathological
CC   conditions which include cancer, diabetic retinopathy, corneal graft
CC   neovascularisation and neovascular glaucoma, epithelial conditions such
CC   as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic
CC   lupus erythematosus, and neurodegenerative diseases. The present sequence
CC   is a RT-PCR primer Mcl-1-R7, used for the amplification of the human
CC   Mcl-1 cDNA.
XX
SQ   Sequence 21 BP; 1 A; 8 C; 2 G; 10 T; 0 other;

Qy   1230 GAAAAGCAAGTGGCAAGAGGA 1250
          |||||||||||||||||||||
Db     21 GAAAAGCAAGTGGCAAGAGGA 1


Query Match             0.5%;  Score 21;  DB 22;  Length 21;
Best Local Similarity   100.0%;  Pred. No. 17;
Matches   21;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 7
AAT03166/c
ID   AAT03166 standard; DNA; 20 BP.
XX
AC   AAT03166;
XX
DT   05-JUN-1996  (first entry)
XX
DE   Human Mcl-1 gene reverse PCR primer.
XX
KW   Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel;
     detection; ss.
XX
OS   Synthetic.
XX
PN   WO9528497-A1.
XX
PD   26-OCT-1995.
XX
PF   12-APR-1995;   95WO-US04600.
PR   13-APR-1994;   94US-0226876.
XX
PA   (LJOL-) LA JOLLA CANCER RES FOUND.
PI   Reed JC, Sato T;
XX
DR   WPI; 1995-373811/48.
XX
PT   Detection of novel proteins involved in apoptosis - by interaction
     with proteins involved in apoptosis.
XX
PS   Example 1; Page 23; 62pp; English.
XX
CC   AAT03164-T031366 are primers used for the amplification of the human
CC   Mcl-1 gene. The Mcl-1 protein is a Bcl-2 related protein, the Mcl-1
CC   protein was expressed and used to investigate the interactions of
CC   Mcl-1 with other proteins known to be involved in apoptosis
CC   (excluding the Bax protein). Proteins detected using this method can
CC   act as upstream activators or downstream effectors of a cellular
CC   protein such as Bax which induces apoptosis. If the protein is a
CC   Bcl-2 related protein apoptosis levels are decreased due to the
CC   protein binding to and inactivating Bax.
XX
SQ   Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Qy   1182 GGACTCCAAGCTGTAACTTC 1201
          ||||||||||||||||||||
Db     20 GGACTCCAAGCTGTAACTTC 1


Query Match             0.5%;  Score 20;  DB 16;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 51;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 8
AAZ39083/c
ID   AAZ39083 standard; DNA; 20 BP.
XX
AC   AAZ39083;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20407.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
     mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
     inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;   99US-0226568.
PR   07-JAN-1999;   99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
     anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
     and treating associated diseases e.g. cancer -
XX
PS   Claim 31; Column 33; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human mcl-1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 other;
```

```
Query Match
Best Local Similarity  100.0%;        0.5%;  Score 20;  DB 21;  Length 20;
                                      Pred. No. 51;
Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   501 CGGGGAATCTGGTAATAACA 520
         ||||||||||||||||||||
Db    20 CGGGGAATCTGGTAATAACA 1

RESULT 9
AA239084/c
ID   AA239084 standard; DNA; 20 BP.
XX
AC   AA239084;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20408.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;    99US-0226568.
XX
PR   07-JAN-1999;    99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ,  Marcusson EG,  Bennett CF,  Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 31; Column 33; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human mcl-1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 0 A; 4 C; 7 G; 9 T; 0 other;


Query Match
Best Local Similarity  100.0%;        0.5%;  Score 20;  DB 21;  Length 20;
                                      Pred. No. 51;
Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   636 CGCCAAGGACACAAAGCCAA 655
         ||||||||||||||||||||
Db    20 CGCCAAGGACACAAAGCCAA 1

RESULT 10
AA239085/c
ID   AA239085 standard; DNA; 20 BP.
XX
AC   AA239085;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20416.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;    99US-0226568.
XX
PR   07-JAN-1999;    99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ,  Marcusson EG,  Bennett CF,  Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Claim 31; Column 33; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human mcl-1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 other;
XX


Query Match
Best Local Similarity  100.0%;        0.5%;  Score 20;  DB 21;  Length 20;
                                      Pred. No. 51;
Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  2366 GGTGGATGGAGAGACATTTG 2385
         ||||||||||||||||||||
Db    20 GGTGGATGGAGAGACATTTG 1

RESULT 11
AA239086/c
ID   AA239086 standard; DNA; 20 BP.
XX
AC   AA239086;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20420.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
```

RESULT 12
AA239087/c
ID   AA239087 standard; DNA; 20 BP.
XX
AC   AA239087;
XX
DT   29-FEB-2000   (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20421.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PS   Claim 31; Column 33; 28pp; English.
XX
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human mcl-1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 other;

Query Match   0.5%; Score 20; DB 21; Length 20;
Best Local Similarity   100.0%;
Matches   20; Conservative   0; Pred. No. 51; Mismatches   0; Indels   0; Gaps   0;

```
Qy       3207 TGTAATGGGGAAGAACTGCC 3226
              ||||||||||||||||||||
Db         20 TGTAATGGGGAAGAACTGCC 1
```

RESULT 13
AA239090/c
ID   AA239090 standard; DNA; 20 BP.
XX
AC   AA239090;
XX
DT   29-FEB-2000   (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20404.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI; 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Example 12; Column 33; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
XX
SQ   Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 other;

Query Match   0.5%; Score 20; DB 21; Length 20;
Best Local Similarity   100.0%;
Matches   20; Conservative   0; Pred. No. 51; Mismatches   0; Indels   0; Gaps   0;

```
Qy       3391 TAAAAGCCTGTCTGCCAAAT 3410
              ||||||||||||||||||||
Db         20 TAAAAGCCTGTCTGCCAAAT 1
```

RESULT 14
AAZ39091/c
ID   AAZ39091 standard; DNA; 20 BP.
XX
AC   AAZ39091;
XX
DT   29-FEB-2000   (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20405.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI: 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Example 12; Column 33; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human mcl-1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 5 A; 8 C; 4 G; 3 T; 0 other;

  Query Match   0.5%; Score 20; DB 21; Length 20;
  Best Local Similarity   100.0%;   Pred. No. 51;
  Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   50 GGGGACTGGCAATGTTTGGC 69
               ||||||||||||||||||||
Db   20 GGGGACTGGCAATGTTTGGC 1

SQ   Sequence 20 BP; 5 A; 9 C; 4 G; 2 T; 0 other;

  Query Match   0.5%; Score 20; DB 21; Length 20;
  Best Local Similarity   100.0%;   Pred. No. 51;
  Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   152 CGGGAGGGCCGACTTTTGGCT 171
               |||||||||||||||||||||
Db   20 CGGGAGGGCCGACTTTTGGCT 1

RESULT 15
AAZ39092/c
ID   AAZ39092 standard; DNA; 20 BP.
XX
AC   AAZ39092;
XX
DT   29-FEB-2000   (first entry)
XX
DE   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20406.
XX
KW   Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW   mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW   inflammation; diagnosis; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6001992-A.
XX
PD   14-DEC-1999.
XX
PF   07-JAN-1999;   99US-0226568.
XX
PR   07-JAN-1999;   99US-0226568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR   WPI: 2000-061908/05.
XX
PT   Antisense oligonucleotides which modulate the expression of novel
PT   anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT   and treating associated diseases e.g. cancer -
XX
PS   Example 12; Column 33; 28pp; English.
XX
CC   The present invention describes antisense oligonucleotides which modulate
CC   the expression of novel anti-apoptotic bcl-2-related proteins. The
CC   antisense oligonucleotides can be used as therapeutic agents to prevent
CC   or delay inflammation or tumour formation by promoting apoptosis in
CC   human cells or tissues. They can also be used as research agents to
CC   establish the function of particular genes and as diagnostic agents in
CC   sandwich assays for detecting the level of novel anti-apoptotic
CC   bcl-2-related proteins in a sample. The antisense oligonucleotides
CC   given in the present invention were designed to target human A1 and
CC   mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC   present sequence represents an antisense oligonucleotide for the
CC   human mcl-1 nucleotide sequence.
XX
SQ   Sequence 20 BP; 2 A; 10 C; 3 G; 5 T; 0 other;

  Query Match   0.5%; Score 20; DB 21; Length 20;
  Best Local Similarity   100.0%;   Pred. No. 51;
  Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   431 AGGAGCTGGACGCGGGTTACGAG 450
               |||||||||||||||||||||
Db   20 AGGAGCTGGACGCGGGTTACGAG 1

Search completed: March 14, 2003, 04:46:54

Job time : 579.329 secs

```
OM nucleic - nucleic search, using sw model

                               GenCore version 5.1.4.p5_4578
                               Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:          March 14, 2003, 04:32:49 ; Search time 732.181 Seconds
                                              (without alignments)
                                 17253.226 Million cell updates/sec

Title:
Perfect score:   780
Sequence:        1 gagtgagcattccagcaca.........aattgtatgtattttctct 780
Scoring table:   OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0
Searched:        16154066 seqs, 8097743376 residues
Word size :      0
Total number of hits satisfying chosen parameters:    102860
Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :       EST:*
                 1: en_estba:*
                 2: en_esthum:*
                 3: en_estin:*
                 4: en_estmu:*
                 5: en_estov:*
                 6: en_estpl:*
                 7: en_estro:*
                 8: en_htc:*
                 9: en_estl:*
                10: gb_est2:*
                11: gb_htc:*
                12: gb_est3:*
                13: gb_est4:*
                14: gb_est5:*
                15: en_estfun:*
                16: en_estom:*
                17: gb_gss:*
                18: en_gss_hum:*
                19: en_gss_inv:*
                20: en_gss_pln:*
                21: en_gss_vrt:*
                22: en_gss_fun:*
                23: en_gss_mam:*
                24: en_gss_mus:*
                25: en_gss_other:*
                26: en_gss_pro:*
                27: en_gss_rod:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result              %
No.  Score  Query       DB       ID         Description
            Match Length
---- -----  -----------  ----     --------   -----------
c 1   28    3.6   43      9       AI370619   AI370619 ta40f05.x
c 2   16    2.1   46     17       BH635174   BH635174 1008002H1
c 3   15    1.9   43     14       C01095     C01095 HUMGS000775
c 4   14    1.8   26     17       AZ439313   AZ439313 1M0229320
c 5   13    1.7   25     17       BH855488   BH855488 SALK_0850
c 6   13    1.7   25     17       TA23F08P   AL453160 T. brucei
```

ALIGNMENTS

```
RESULT 1
AI370619/c
LOCUS       AI370619          43 bp    mRNA    linear    EST 16-FEB-1999
DEFINITION  AI370619 ta40f05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
            IMAGE:2046561 3' similar to SW:BFL1_HUMAN Q16548 BCL2-RELATED
            PROTEIN A1 ;contains element TAR1 repetitive element ;; mRNA
            sequence.
ACCESSION   AI370619
VERSION     AI370619.1       GI:4149372
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 431   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..43
```

```
c  7   13  1.7   26   9   17   AZ787019   AZ787019 2M0032B19
   8   13  1.7   29  17        AZ323085   AZ323085 1M0044J02
   9   13  1.7   30   9        AL761633   AL761633 Arabidops
  10   13  1.7   31  17        AZ809484   AZ809484 2M0073F04
  11   13  1.7   33   9        AU240558   AU240558 AU240558
  12   13  1.7   35   9        AU009945   AU009945 AU009945
  13   13  1.7   36  17        AZ482026   AZ482026 1M0306K18
  14   13  1.7   36  17        BH849581   BH849581 SALK_0699
  15   13  1.7   38  17        AL762626   AL762626 Arabidops
  16   13  1.7   40  17        BH011458   BH011458 BG02105-5
c 17   13  1.7   43   9        AA253295   AA253295 zr71g08.r
  18   13  1.7   43  17        BH792796   BH792796 SALK_0650
  19   13  1.7   45  17        AZ389050   AZ389050 1M0149E19
  20   13  1.7   46   9        AA920919   AA920919 vy15a07.r
  21   13  1.7   46  14        N77017     N77017 yz83b09.r1
  22   13  1.7   47  14        C00031     C00031 HUMGS000334
  23   13  1.7   48  17        AZ946920   AZ946920 2M0208L19
  24   13  1.7   50   9        AU104419   AU104419 AU104419
c 25   13  1.7   50  14        BM733456   BM733456 kj33d03.y
c 26   13  1.7   19  17        AZ346703   AZ346703 1M0082L05
c 27   13  1.7   21  17        AZ508369   AZ508369 1M0350A24
  28   12  1.5   21  17        AZ816467   AZ816467 2M0085B14
  29   12  1.5   22  17        AZ786328   AZ786328 2M0031G14
c 30   12  1.5   23  17        AZ462638   AZ462638 1M0269L08
  31   12  1.5   24   9        AU260073   AU260073 AU260073
  32   12  1.5   25  17        AZ845871   AZ845871 2M0145B19
  33   12  1.5   26  17        BH754276   BH754276 SALK_0392
  34   12  1.5   27  13        BM395315   BM395315 50072-2-8
  35   12  1.5   28   9        AI153397   AI153397 uc52e05.r
c 36   12  1.5   29  14        D45819     D45819 HUMGS03038
  37   12  1.5   30   9        AU257038   AU257038 AU257038
  38   12  1.5   30   9        AU259737   AU259737 AU259737
c 39   12  1.5   30  10        AW332749   AW332749 S12E1 AGS
  40   12  1.5   31  17        AZ346753   AZ346753 1M0082E11
c 41   12  1.5   32   9        BH863143   BH863143 SALK_0932
  42   12  1.5   32  17        AU254252   AU254252 AU254252
  43   12  1.5   32  17        AZ331642   AZ331642 1M0059P11
  44   12  1.5   32  17        AZ469379   AZ469379 1M0282P14
  45   12  1.5   32  17        AZ663912   AZ663912 1M0543J18
```

```
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2046561"
                     /clone_lib="Soares_total_fetus_Nb2HF8_9w"
                     /dev_stage="8-9 weeks"
                     /lab_host="DH10b"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from pooled 8-9 week
                     (total) fetus material with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGACGAGCGGCCGCCTTAATTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT      13 a      11 c       7 g      12 t
ORIGIN

Qy     526  CCTAAAATCTGGCTGGATGAGACTTTTCTAG 553
            ||||||||||||||||||||||||||||||
Db      28  CCTAAAATCTGGCTGGATGAGACTTTTCTAG 1


RESULT 2

Query Match             100.0%;     Score 16;     DB 17;     Length 46;
Best Local Similarity   2.1%;       Pred. No. 1.3e+03;
Matches    16;          Conservative    0;     Mismatches    0;     Indels    0;     Gaps    0;

LOCUS       BH635174      46 bp    DNA      linear   GSS 14-FEB-2002
DEFINITION  1008002H10.2EL_x1 1008 - RescueMu Grid I zea mays genomic, DNA
            sequence.
ACCESSION   BH635174
VERSION     BH635174.1  GI:18657411
KEYWORDS    GSS.
SOURCE      Zea mays.
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 46)
AUTHORS     Walbot,V.
TITLE       Maize genomic sequences found using engineered RescueMu transposon
JOURNAL     Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1008002 row: 36
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1..46
                     /organism="zea mays"
                     /cultivar="mixed background W23/A188/B73"
                     /db_xref="taxon:4577"
                     /clone_lib="1008 - RescueMu Grid I"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site www.zmdb.iastate.edu and follow the links for
                     'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
                     extracted from leaf punches, double digested using BamHI
                     and BglII, and ligated to form circular plasmids. DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."

BASE COUNT      17 a       3 c       6 g      20 t
ORIGIN

Qy      90  TGAATTGGATATATT 105
            |||||||||||||||
Db      24  TGAATTGGATATATT 39


RESULT 3

Query Match             100.0%;     Score 15;     DB 14;     Length 43;
Best Local Similarity   1.9%;       Pred. No. 4.7e+03;
Matches    15;          Conservative    0;     Mismatches    0;     Indels    0;     Gaps    0;

LOCUS       C01095        43 bp    mRNA     linear   EST 23-JUL-1996
DEFINITION  HUMGS0007755 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   C01095
VERSION     C01095.1  GI:1433325
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
AUTHORS     Okubo,K.
TITLE       BodyMap; human gene expression database
JOURNAL     Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            Human Gene Signature, 3'-directed cDNA sequence. We are not
            submitting the same cDNA sequence redundantly to DDBJ since 1993.
            For the abundance information of clones with this sequence in this
            library and as well as in other 3'-directed libraries, see
            http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones
            represented by this GS sequences is also found there.
FEATURES             Location/Qualifiers
     source          1..43
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human adult (K.Okubo)"
                     /dev_stage="adult"
                     /note="Organ: blood; Vector: 1-gt-11; Site_1: Eco-RI;
                     Monocytes were prepared from blood by ficoll-hypaque,
                     percoll and T cell rosetting purification steps (purity:
                     96 %). mRNA was prepared from activated monocytes from a
                     patient with rheumatoid arthritis. mRNA was reverse
                     transcribed with MuLV. Using Eco-RI linkers cDNA was
                     cloned into 1-gt-11 vector arms. The cDNA library was
                     screened by differential hybidization using radioactively
                     marked ss-cDNA from activated and non-activated
                     monocytes."

BASE COUNT      15 a       9 c       4 g      15 t
ORIGIN

Qy     496  TGGGAAAAATGGCTTT 510
            ||||||||||||||||
Db      42  TGGGAAAAATGGCTTT 28


RESULT 4
```

```
A2439313
LOCUS       A2439313       26 bp    DNA    linear    GSS 03-OCT-2000
DEFINITION  IM0229320R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
            clone UUGC1M0229J20 R, DNA sequence.
ACCESSION   A2439313
VERSION     A2439313.1  GI:10563326
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 26)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7117
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0229 row: J column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1..26
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0229J20"
                     /clone_lib="Mouse 10kb plasmid UUGCIM library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|14732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT     12 a   5 c   2 g   7 t
ORIGIN

RESULT 5

Qy          719  ACCTTCCAGAGTTA  732
                 ||||||||||||||
Db            7  ACCTTCCAGAGTTA  20

Query Match     1.8%;  Score 14;  DB 17;  Length 26;
Best Local Similarity  100.0%;  Pred. No. 1.4e+04;
Matches   14;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
BH855488
LOCUS       BH855488       25 bp    DNA    linear    GSS 08-JUL-2002
DEFINITION  SALK_085052.22.25.x Arabidopsis thaliana TDNA insertion lines
            clone SALK_085052.22.25.x, DNA
            sequence.
ACCESSION   BH855488
VERSION     BH855488.1  GI:21705078
KEYWORDS    GSS.
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
TITLE       A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL     Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1..25
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_085052.22.25.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      6 a   1 c   5 g   13 t
ORIGIN

RESULT 6

Qy          760  AAATTGTATGTAT  772
                 |||||||||||||
Db           12  AAATTGTATGTAT  24

Query Match     1.7%;  Score 13;  DB 17;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 5.1e+04;
Matches   13;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

TA23F08P/c
LOCUS       TA23F08P       25 bp    DNA    linear    GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 23f08, forward sequence,
            genomic survey sequence.
ACCESSION   AL453160
VERSION     AL453160.1  GI:11847458
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
ORGANISM    Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE       Direct Submission
JOURNAL     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
```

```
COMMENT     project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
         source          1..25
                         /organism="Trypanosoma brucei"
                         /strain="TREU927"
                         /db_xref="taxon:5691"
                         /clone="23f08"
BASE COUNT       11 a       4 c       4 g       6 t
ORIGIN

Qy  287  TATTCAACCAAGT  299
         |||||||||||||
Db   20  TATTCAACCAAGT    8

Query Match            1.7%;  Score 13;  DB 17;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 5.1e+04;
Matches  13;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 7
AZ787019
LOCUS       AZ787019          26 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0032B19R Mouse 10kb plasmid UUGC2M0032B19 R, DNA sequence.
ACCESSION   AZ787019
VERSION     AZ787019.1  GI:12925362
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0032   row: B   column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
         source          1..26
                         /organism="Mus musculus"
                         /strain="C57BL/6J"
                         /db_xref="taxon:10090"
                         /clone="UUGC2M0032B19"
                         /clone_lib="Mouse 10kb plasmid UUGC2M0032B19 library"
                         /sex="Male"
                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                         /note="Vector: PWD42nv; Purified genomic DNA from M.
                         musculus C57BL/6J (male) was obtained from the Jackson
                         Laboratory Mouse DNA Resource
                         (http://www.jax.org/resources/documents/dnares/). The DNA
                         was hydrodynamically sheared by repeated passage through a
                         0.005 inch orifice at constant velocity. The sheared DNA
                         was blunt end-repaired with T4 DNA polymerase and T4
                         polynucleotide kinase. Adaptor oligonucleotides were
                         ligated to the blunt ends in high molar excess. The
                         adaptored DNA was purified and size-selected for a 9.5 to
                         10.5 kb range using preparative agarose gel
                         electrophoresis. Vector DNA was prepared from a derivative
                         of pWD42 (gi|47321141|gb|AF129072.1), a copy-number
                         inducible derivative of plasmid R1. The vector was ligated
                         with adaptors complementary to the insert adaptors and
                         purified. The sheared, adaptored mouse DNA was annealed to
                         adaptored vector DNA, and transformed into
                         chemically-competent E. coli XL10-Gold (Stratagene) cells
                         and selected for ampicillin resistance."
BASE COUNT        9 a       9 c       4 g       4 t
ORIGIN

Qy   65  CCACCAGGCAGAA  77
         |||||||||||||
Db    4  CCACCAGGCAGAA  16

Query Match            1.7%;  Score 13;  DB 17;  Length 26;
Best Local Similarity  100.0%;  Pred. No. 5.1e+04;
Matches  13;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 8
AZ323085/c
LOCUS       AZ323085          29 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0044J02F Mouse 10kb plasmid UUGC1M0044J02 F, DNA sequence.
ACCESSION   AZ323085
VERSION     AZ323085.1  GI:10377460
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0044   row: J   column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
         source          1..29
                         /organism="Mus musculus"
                         /strain="C57BL/6J"
                         /db_xref="taxon:10090"
                         /clone="UUGC1M0044J02"
                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
```

RESULT 9

LOCUS   AL761633   30 bp   DNA   linear   GSS 18-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-227B05-014266,
            genomic survey sequence.
ACCESSION   AL761633
VERSION   AL761633.1 GI:21504571
KEYWORDS   GSS.
SOURCE   thale cress.
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 30)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE   A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
  TITLE   A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 30)
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT   This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone MPI21. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics Program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpi-koeln.mpg.de/GABI-Kat/.
FEATURES   Location/Qualifiers
     source   1..30
                     /organism="Arabidopsis thaliana"

Qy   613 AGGACACTCCATA 625
                |||||||||||||
Db   22 AGGACACTCCATA 10

BASE COUNT   2 a   6 c   11 g   10 t
ORIGIN

Query Match   1.7%; Score 13; DB 17; Length 29;
Best Local Similarity   100.0%; Pred. No. 5.3e+04;
Matches   13; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 10

LOCUS   AZ809484   31 bp   DNA   linear   GSS 20-FEB-2001
DEFINITION 2M0073F04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
            clone UUGC2M0073F04 R, DNA sequence.
ACCESSION   AZ809484
VERSION   AZ809484.1 GI:12975843
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0073 row: F column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES   Location/Qualifiers
     source   1..31
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0073F04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD4nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     /clone_lib="Mouse 10kb plasmid UUGCIM library"

Qy   306 AAAGGAGTTTGAA 318
                |||||||||||||
Db   10 AAAGGAGTTTGAA 22

BASE COUNT   12 a   3 c   7 g   8 t
ORIGIN

Query Match   1.7%; Score 13; DB 17; Length 30;
Best Local Similarity   100.0%; Pred. No. 5.4e+04;
Matches   13; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|1473211|4|gb|AF129072.1|), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
ORIGIN
BASE COUNT     14 a     7 c     7 g     3 t

Qy   135 CGTCCTACAGATA 147
         |||||||||||||
Db     4 CGTCCTACAGATA 16

Best Local Similarity     100.0%;
Matches     13;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;

Query Match     1.7%;   Score 13;   DB 17;   Length 31;
Pred. No. 5.4e+04;
```

RESULT 11
```
LOCUS       AU240558                33 bp    mRNA    linear   EST 15-JAN-2002
DEFINITION  AU240558 UV irradiated OLHNI cell line cDNA library (OLc) Oryzias
            latipes cDNA clone OLc21.11d, mRNA sequence.
ACCESSION   AU240558
VERSION     AU240558.1  GI:18151337
KEYWORDS    EST.
SOURCE      Japanese medaka.
ORGANISM    Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Naruse,K., Mitani,H. and Tanaka,M.
  TITLE     Medaka EST Project in University of Tokyo (2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kiyoshi Naruse
            Department of Biological Sciences
            Graduate School of Science, University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
            Tel: 81-3-5841-4443
            Fax: 81-3-5841-4410
            Email: naruse@biol.s.u-tokyo.ac.jp
            This clone was isolated from UV irradiated OLHNI cell line cDNA
            library (OLc) 5' end sequences.
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="Oryzias latipes"
                     /strain="HNI"
                     /db_xref="taxon:8090"
                     /clone="OLc21.11d"
                     /clone_lib="UV irradiated OLHNI cell line cDNA library (OLc)"
ORIGIN
BASE COUNT     10 a     9 c     5 g     8 t     1 others

Qy    26 TCAACAGCTTCAA 38
         |||||||||||||
Db    16 TCAACAGCTTCAA 28

Best Local Similarity     100.0%;
Matches     13;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;

Query Match     1.7%;   Score 13;   DB 9;   Length 33;
Pred. No. 5.6e+04;
```

RESULT 12
```
LOCUS       AU009945                35 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU009945 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc00705, mRNA sequence.
ACCESSION   AU009945
VERSION     AU009945.1  GI:3346625
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe
ORGANISM    Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1..35
                     /organism="Schizosaccharomyces pombe"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc00705"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /sex="h minus"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web. (URL, http://www.nirs.go.jp)"
ORIGIN
BASE COUNT     19 a     2 c     6 g     8 t

Qy    99 ATATATTTACAGG 111
         |||||||||||||
Db     8 ATATATTTACAGG 20

Best Local Similarity     100.0%;
Matches     13;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;

Query Match     1.7%;   Score 13;   DB 9;   Length 35;
Pred. No. 5.7e+04;
```

RESULT 13
```
LOCUS       AZ482026                36 bp    DNA    linear   GSS 04-OCT-2000
DEFINITION  IM0306K18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0306K18 R, DNA sequence.
ACCESSION   AZ482026
VERSION     AZ482026.1  GI:10643091
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,T., Pedersen,T., Reilly,
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
```

```
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000   Std Error: 0.00
Plate: 0306  row: K  column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1..36
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0306K18"
                     /sex="Male"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|14732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      4 c     16 g      10 t
ORIGIN

RESULT 14
BH849581
LOCUS       BH849581               36 bp    DNA     linear   GSS 13-JUN-2002
DEFINITION  SALK_069905.21.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_069905.21.55.x, DNA
            sequence.
ACCESSION   BH849581
VERSION     BH849581.1  GI:21420452
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Kanes,M., Kim,C.J., Parker,H., Predais,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            The Salk Institute Genomic Analysis Laboratory (SIGnAL)
            Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
```

```
Qy          438 TTTTGTTCGGGAG 450
                ||||||||||||||
Db            2 TTTTGTTCGGGAG 14
```

Query Match   1.7%; Score 13; DB 17; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
TDNA. This single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At5g15570.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1..36
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_069905.21.55.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT        8 a      1 c     11 g      15 t      1 others
ORIGIN
```

Query Match   1.7%; Score 13; DB 17; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          334 TGGGGAAGAATTG 346
                |||||||||||||
Db           15 TGGGGAAGAATTG 27
```

```
RESULT 15
AL762626
LOCUS       AL762626               38 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-026F02-013759,
            genomic survey sequence.
ACCESSION   AL762626
VERSION     AL762626.1  GI:21509038
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 38)
  AUTHORS   Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene Atig29750. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1..38
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
```

```
                    /db_xref="taxon:3702"
                    /clone="GK-026F02-013759"
                    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                    /note="PCR was performed on DNA from Arabidopsis thaliana
                    plants (T1) which were transformed with the T-DNA from
                    vector pAC106. The lines contain one or more T-DNA
                    insertions. The DNA fragment(s) resulting from the PCR
                    were directly sequenced to determine the genomic sequence
                    flanking the insertion. Sequences displaying significant
                    similarity to the A. thalaina nuclear genome sequence were
                    processed for submission. T-DNA derived sequences were
                    removed"
```

BASE COUNT   9 a   4 c   9 g   16 t
ORIGIN

Query Match   1.7%;   Score 13;   DB 17;   Length 38;
Best Local Similarity   100.0%;   Pred. No. 5.8e+04;
Matches   13;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy    433 TCATATTTGTTG 445
          ||||||||||||
Db      7 TCATATTTGTTG 19
```

Search completed: March 14, 2003, 08:29:33
Job time : 738.181 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 04:33:38 ; Search time 95.137 seconds
(without alignments)
12681.353 Million cell updates/sec

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccagtaaggagtcgggtc..........aaatctttattcaaataa 3934

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	0.5	21	1	US-08-607-269-1	Sequence 1, Appli
2	21	0.5	21	5	PCT-US95-04600-1	Sequence 1, Appli
3	20	0.5	20	1	US-08-607-269-3	Sequence 3, Appli
4	20	0.5	20	5	PCT-US92-09202-6	Sequence 6, Appli
5	20	0.5	20	5	PCT-US93-07743-5	Sequence 5, Appli
6	20	0.5	20	3	US-09-226-568-20	Sequence 19, Appli
7	20	0.5	20	3	US-09-226-568-21	Sequence 20, Appli
8	20	0.5	20	3	US-09-226-568-22	Sequence 21, Appli
9	20	0.5	20	3	US-09-226-568-23	Sequence 22, Appli
10	20	0.5	20	3	US-09-226-568-24	Sequence 23, Appli
11	20	0.5	20	3	US-09-226-568-25	Sequence 24, Appli
12	20	0.5	20	3	US-09-226-568-26	Sequence 25, Appli
13	20	0.5	20	3	US-09-226-568-27	Sequence 26, Appli
14	20	0.5	20	3	US-09-226-568-28	Sequence 27, Appli
15	20	0.5	20	3	US-09-226-568-29	Sequence 28, Appli
16	20	0.5	20	3	US-09-226-568-30	Sequence 29, Appli
17	20	0.5	20	3	US-09-226-568-31	Sequence 30, Appli
18	20	0.5	20	3	US-09-226-568-32	Sequence 31, Appli
19	20	0.5	20	3	US-09-226-568-33	Sequence 32, Appli
20	20	0.5	20	3	US-09-226-568-34	Sequence 33, Appli
21	20	0.5	20	3	US-09-226-568-35	Sequence 34, Appli
22	20	0.5	20	3	US-09-226-568-36	Sequence 35, Appli
23	20	0.5	20	3	US-09-226-568-37	Sequence 36, Appli
24	20	0.5	20	3	US-09-226-568-38	Sequence 38, Appli
25	18	0.5	20	5	PCT-US95-04600-3	Sequence 3, Appli
26	18	0.5	26	1	US-08-607-269-17	Sequence 17, Appli
27	18	0.5	28	5	PCT-US92-09202-7	Sequence 7, Appli
28	18	0.5	18	3	US-08-607-269-1	Sequence 1, Appli
29	18	0.5	18	2	US-08-857-946-106	Sequence 105, App
30	18	0.5	38	3	US-08-970-740-106	Sequence 106, App
31	18	0.5	41	5	PCT-US92-09202-6	Sequence 6, Appli
32	18	0.5	41	5	PCT-US93-07743-5	Sequence 5, Appli
33	18	0.5	41	5	PCT-US93-07743-10	Sequence 10, Appli
34	17	0.4	24	1	US-08-607-269-16	Sequence 16, Appli
35	17	0.4	24	5	PCT-US95-04600-16	Sequence 16, Appli
36	17	0.4	28	5	PCT-US95-04600-17	Sequence 17, Appli
37	17	0.4	41	5	PCT-US92-09202-4	Sequence 4, Appli
38	16	0.4	19	4	US-09-177-953-9	Sequence 9, Appli
39	16	0.4	21	2	US-08-863-6399A-36	Sequence 36, Appli
40	16	0.4	21	2	US-08-863-6399A-48	Sequence 48, Appli
41	16	0.4	21	2	US-08-863-6399A-50	Sequence 50, Appli
42	16	0.4	21	2	US-08-863-6399A-73	Sequence 73, Appli
43	16	0.4	21	2	US-08-863-6399A-76	Sequence 76, Appli
44	16	0.4	21	2	US-08-863-6399A-88	Sequence 88, Appli
45	16	0.4	24	1	US-08-160-670A-49	Sequence 49, Appli

ALIGNMENTS

RESULT 1
US-08-607-269-1/c
Sequence 1, Application US/08607269
Patent No. 5702897
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 435.
FILING DATE:
CLASSIFICATION: 435.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-607-269-1

Query Match 100.0%; Score 21; DB 1; Length 21;
    0.5%; Pred. No. 3.3;
Best Local Similarity 100.0%;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1235 GCAAGTGGCGAAGAGGATTATG 1255
         |||||||||||||||||||||
```

Db   21 GCAAGTGGCAAGAGGATTATG 1

RESULT 2
PCT-US95-04600-1/c
; Sequence 1, Application PCT/US9504600
; GENERAL INFORMATION:
;   APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
;   TITLE OF INVENTION: Interaction of Proteins Involved in
;   TITLE OF INVENTION: a Cell Death Pathway
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Campbell and Flores
;   STREET: 4370 La Jolla Village Drive, Suite 700
;   CITY: San Diego
;   STATE: California
;   COUNTRY: USA
;   ZIP: 92122
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/04600
;   FILING DATE: 12-APR-1995
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Imbra, Richard J.
;   REGISTRATION NUMBER: 37,643
;   REFERENCE/DOCKET NUMBER: FP-LJ 1361
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 21 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
PCT-US95-04600-1

Qy   1235 GCAAGTGGCAAGAGGATTATG 1255
             |||||||||||||||||||||
Db   21 GCAAGTGGCAAGAGGATTATG 1

Query Match   0.5%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-08-607-269-3/c
; Sequence 3, Application US/0860726 9
; Patent No. 5702897
; GENERAL INFORMATION:
;   APPLICANT: Reed, John C.
;   APPLICANT: Sato, Takaaki
;   TITLE OF INVENTION: Interaction of Proteins Involved in a
;   TITLE OF INVENTION: Cell Death Pathway
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Campbell and Flores
;   STREET: 4370 La Jolla Village Drive, Suite 700
;   CITY: San Diego
;   STATE: California
;   COUNTRY: USA
;   ZIP: 92122
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25

;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/607,269
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/226,876
;   FILING DATE: 13-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Campbell, Cathryn A.
;   REGISTRATION NUMBER: 31,815
;   REFERENCE/DOCKET NUMBER: P-LJ 9882
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-607-269-3

Qy   1182 GGACTCCAAGCTGTAACTTC 1201
             ||||||||||||||||||||
Db   20 GGACTCCAAGCTGTAACTTC 1

Query Match   0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-226-568-19/c
; Sequence 19, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
;   APPLICANT: Ackermann, Elizabeth J.
;   APPLICANT: Bennett, C. Frank
;   APPLICANT: Dean, Nicholas M.
;   APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-226-568-19

Qy   50 GGCGACTGGCAATGTTTGGC 69
             ||||||||||||||||||||
Db   20 GGCGACTGGCAATGTTTGGC 1

Query Match   0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-226-568-20/c
; Sequence 20, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
;   APPLICANT: Ackermann, Elizabeth J.
;   APPLICANT: Bennett, C. Frank
;   APPLICANT: Dean, Nicholas M.

```
RESULT 6
US-09-226-568-21/c
Sequence 21, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
  APPLICANT: Ackermann, Elizabeth J.
  APPLICANT: Bennett, C. Frank
  APPLICANT: Dean, Nicholas M.
  APPLICANT: Marcusson, Eric G.
  TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
  TITLE OF INVENTION: bcl-2-Related Proteins
  FILE REFERENCE: ISPH-0337
  CURRENT APPLICATION NUMBER: US/09/226,568
  CURRENT FILING DATE: 1999-01-07
  NUMBER OF SEQ ID NOS: 39
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
  LENGTH: 20
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: antisense
  OTHER INFORMATION: sequence
US-09-226-568-21

Qy     152  CGGGGAGGCGGCGACTTTTGGCT 171
            |||||||||||||||||||||
Db      20  CGGGGAGGCGGCGACTTTTGGCT 1

Query Match          0.5%;     Score 20;   DB 3;     Length 20;
Best Local Similarity  100.0%;  Pred. No. 9.8;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


RESULT 7
US-09-226-568-22/c
Sequence 22, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
  APPLICANT: Ackermann, Elizabeth J.
  APPLICANT: Bennett, C. Frank
  APPLICANT: Dean, Nicholas M.
  APPLICANT: Marcusson, Eric G.
  TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
  TITLE OF INVENTION: bcl-2-Related Proteins
  FILE REFERENCE: ISPH-0337
  CURRENT APPLICATION NUMBER: US/09/226,568
  CURRENT FILING DATE: 1999-01-07
  NUMBER OF SEQ ID NOS: 39
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
  LENGTH: 20
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: antisense
  OTHER INFORMATION: sequence
US-09-226-568-22

Qy     501  CGGGGAATCTGGTAATAACA 520
            ||||||||||||||||||||
Db      20  CGGGGAATCTGGTAATAACA 1

Query Match          0.5%;     Score 20;   DB 3;     Length 20;
Best Local Similarity  100.0%;  Pred. No. 9.8;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


RESULT 8
US-09-226-568-23/c
Sequence 23, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
  APPLICANT: Ackermann, Elizabeth J.
  APPLICANT: Bennett, C. Frank
  APPLICANT: Dean, Nicholas M.
  APPLICANT: Marcusson, Eric G.
  TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
  TITLE OF INVENTION: bcl-2-Related Proteins
  FILE REFERENCE: ISPH-0337
  CURRENT APPLICATION NUMBER: US/09/226,568
  CURRENT FILING DATE: 1999-01-07
  NUMBER OF SEQ ID NOS: 39
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
  LENGTH: 20
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: antisense
  OTHER INFORMATION: sequence
US-09-226-568-23

Qy     636  CGCCAAGGACACAAAGCCAA 655
            ||||||||||||||||||||
Db      20  CGCCAAGGACACAAAGCCAA 1

Query Match          0.5%;     Score 20;   DB 3;     Length 20;
Best Local Similarity  100.0%;  Pred. No. 9.8;
Matches   20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


RESULT 9
US-09-226-568-24/c
Sequence 24, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
  APPLICANT: Ackermann, Elizabeth J.
  APPLICANT: Bennett, C. Frank
  APPLICANT: Dean, Nicholas M.
  APPLICANT: Marcusson, Eric G.
  TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
  TITLE OF INVENTION: bcl-2-Related Proteins
  FILE REFERENCE: ISPH-0337
  CURRENT APPLICATION NUMBER: US/09/226,568
  CURRENT FILING DATE: 1999-01-07
  NUMBER OF SEQ ID NOS: 39
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
  LENGTH: 20
```

Qy   431 AGGAGCTGGACGGGGTACGAG 450
            |||||||||||||||||||||
Db   20 AGGAGCTGGACGGGGTACGAG 1

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-24

```
Qy   842 GGGGCAGGATTGTGACTCTC 861
         ||||||||||||||||||||
Db    20 GGGGCAGGATTGTGACTCTC 1
```

Query Match   100.0%; Score 20; DB 3; Length 20;
Best Local Similarity   0.5%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-226-568-25/c
Sequence 25, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-25

```
Qy  1045 AGGAAATGTGCTGCTGGCTTT 1064
         ||||||||||||||||||||
Db    20 AGGAAATGTGCTGCTGGCTTT 1
```

Query Match   100.0%; Score 20; DB 3; Length 20;
Best Local Similarity   0.5%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-09-226-568-26/c
Sequence 26, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-26

```
Qy  1230 GAAAAGCAAGTGGCAAGAGG 1249
         ||||||||||||||||||||
Db    20 GAAAAGCAAGTGGCAAGAGG 1
```

Query Match   100.0%; Score 20; DB 3; Length 20;
Best Local Similarity   0.5%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
US-09-226-568-27/c
Sequence 27, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-27

```
Qy  1519 AAGAATGCCAGTGACCTGTG 1538
         ||||||||||||||||||||
Db    20 AAGAATGCCAGTGACCTGTG 1
```

Query Match   100.0%; Score 20; DB 3; Length 20;
Best Local Similarity   0.5%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-09-226-568-28/c
Sequence 28, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense

```
Qy    1676  GGCTTGGTTCCATGATTCTT 1695
            ||||||||||||||||||||
Db      20  GGCTTGGTTCCATGATTCTT 1

RESULT 14
US-09-226-568-29/c
;   Sequence 29, Application US/09226568
;   Patent No. 6001992
;   GENERAL INFORMATION:
;     APPLICANT: Ackermann, Elizabeth J.
;     APPLICANT: Bennett, C. Frank
;     APPLICANT: Dean, Nicholas M.
;     APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 29
;     LENGTH: 20
;     TYPE: DNA
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: antisense
;     OTHER INFORMATION: sequence
US-09-226-568-29

  Query Match          0.5%;   Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;   Pred. No. 9.8;
  Matches   20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    2091  TGAAAACCTGGGATTGAGAG 2110
            ||||||||||||||||||||
Db      20  TGAAAACCTGGGATTGAGAG 1

RESULT 15
US-09-226-568-30/c
;   Sequence 30, Application US/09226568
;   Patent No. 6001992
;   GENERAL INFORMATION:
;     APPLICANT: Ackermann, Elizabeth J.
;     APPLICANT: Bennett, C. Frank
;     APPLICANT: Dean, Nicholas M.
;     APPLICANT: Marcusson, Eric G.
;   TITLE OF INVENTION: Antisense Modulation of No. 6001992e1 Anti-apoptotic
;   TITLE OF INVENTION: bcl-2-Related Proteins
;   FILE REFERENCE: ISPH-0337
;   CURRENT APPLICATION NUMBER: US/09/226,568
;   CURRENT FILING DATE: 1999-01-07
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 30
;     LENGTH: 20
;     TYPE: DNA
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: antisense
;     OTHER INFORMATION: sequence
US-09-226-568-30

  Query Match          0.5%;   Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;   Pred. No. 9.8;
  Matches   20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    2231  TGAGTTCCTTCCATTTGACC 2250
            ||||||||||||||||||||
Db      20  TGAGTTCCTTCCATTTGACC 1
```

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 07:14:05 ; Search time 247.857 Seconds
                 (without alignments)
                 11140.041 Million cell updates/sec

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccagtaaggagtcgggtc.........aaatctttattcaaataaa 3934

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched :   501302 seqs, 350932545 residues

Word size :   0

Total number of hits satisfying chosen parameters: 282380

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB ID	Description
1	17	0.4	33	US-09-884-814-4	Sequence 4, Appl
2	16	0.4	17	US-09-263-959-900	Sequence 900, App
3	16	0.4	17	US-09-263-959-904	Sequence 904, App
4	16	0.4	18	US-09-263-959-921	Sequence 921, App
5	16	0.4	21	US-09-828-034-11	Sequence 11, Appl
6	16	0.4	10	US-09-828-034-30	Sequence 30, Appl
7	16	0.4	21	US-09-828-034-31	Sequence 31, Appl
8	16	0.4	22	US-10-194-59-12	Sequence 12, Appl
9	16	0.4	9	US-09-814-986-59	Sequence 59, Appl
10	16	0.4	25	US-09-811-824-5	Sequence 5, Appl
11	16	0.4	26	US-09-811-824-5	Sequence 5, Appli
12	16	0.4	9	US-09-045-620-3	Sequence 3, Appli
13	16	0.4	30	US-09-728-466-19	Sequence 19, Appl
14	16	0.4	10	US-09-954-697-50	Sequence 50, Appl
15	16	0.4	33	US-09-817-513A-22	Sequence 22, Appli
16	16	0.4	12	US-10-043-142-4	Sequence 4, Appli
17	16	0.4	9	US-09-996-634-108	Sequence 108, Appl
18	16	0.4	9	US-10-026-914-8	Sequence 8, Appli
19	16	0.4	46	US-10-026-914-10	Sequence 10, Appl
20	16	0.4	46	US-10-026-914-14	Sequence 14, Appl
21	16	0.4	9	US-10-026-914-16	Sequence 16, Appl
22	16	0.4	47	US-10-026-914-4	Sequence 4, Appl
23	16	0.4	48	US-09-801-042-8	Sequence 8, Appli
24	16	0.4	10	US-09-801-042-6	Sequence 6, Appli
25	16	0.4	50	US-09-935-727-206	Sequence 206, Appl
26	15	0.4	18	US-09-969-373-2606	Sequence 2606, Ap
27	15	0.4	27	US-09-873-676-74	Sequence 74, Appl
28	15	0.4	30	US-09-976-736-27	Sequence 27, Appl
29	15	0.4	31	US-09-912-263-155	Sequence 155, Appl
30	15	0.4	44	US-09-007-093-16	Sequence 16, Appl
31	15	0.4	46	US-10-137-316-5	Sequence 5, Appli
32	15	0.4	46	US-10-137-316-7	Sequence 7, Appli
33	14	0.4	19	US-09-961-077-1149	Sequence 1149, Ap
34	14	0.4	10	US-09-736-863-16	Sequence 16, Appl
35	14	0.4	20	US-09-863-806-85	Sequence 85, Appl
36	14	0.4	20	US-09-800-629A-27	Sequence 27, Appl
37	14	0.4	21	US-09-828-034-9	Sequence 9, Appli
38	14	0.4	22	US-09-828-034-28	Sequence 28, Appl
39	14	0.4	23	US-09-263-959-1093	Sequence 1093, Ap
40	14	0.4	10	US-09-735-995-17	Sequence 17, Appl
41	14	0.4	23	US-09-735-995-73	Sequence 73, Appl
42	14	0.4	24	US-09-911-176B-27	Sequence 27, Appl
43	14	0.4	24	US-09-804-717A-30	Sequence 30, Appl
44	14	0.4	24	US-10-180-762-27	Sequence 27, Appl
45	14	0.4	25	US-09-755-088-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-884-814-4

; Sequence 4, Application US/09884814
; Patent No. US20020127600A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-0011100S
; CURRENT APPLICATION NUMBER: US/09,884,814
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:U8R primer
US-09-884-814-4

Query Match   100.0%; Score 17; DB 10; Length 33;
Best Local Similarity   100.0%;
Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   453 GGAGCCTCTCGGGAAGC 469
                |||||||||||||||||
Db   17 GGAGCCTCTCGGGAAGC 33

RESULT 2
US-09-263-959-900

; Sequence 900, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 900:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-900

Qy 1148 ACCACCACCACCACACA 1163
        |||||||||||||||||
Db   1 ACCACCACCACCACACA 16

Query Match   100.0%;   Score 16;   DB 10;   Length 17;
Best Local Similarity   0.4%;   Pred. No. 6.4e+02;
Matches 16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 3
US-09-263-959-904
Sequence 904, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 904:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-904

Qy 1148 ACCACCACCACCACACA 1163
        |||||||||||||||||
Db   2 ACCACCACCACCACACA 17

Query Match   100.0%;   Score 16;   DB 10;   Length 17;
Best Local Similarity   0.4%;   Pred. No. 6.4e+02;
Matches 16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 4
US-09-263-959-921
Sequence 921, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 921:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-921

Qy 1148 ACCACCACCACCACACA 1163
        |||||||||||||||||
Db   1 ACCACCACCACCACACA 16

Query Match   100.0%;   Score 16;   DB 10;   Length 18;
Best Local Similarity   0.4%;   Pred. No. 6.5e+02;
Matches 16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 5
US-09-828-034-11
Sequence 11, Application US/09828034
Patent No. US20020064771A1

GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 11
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-11

Query Match   100.0%;   Pred. No. 6.6e+02;
Best Local Similarity   0.4%;   Score 16;   DB 10;   Length 21;
Matches 16;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1148 ACCACCACCACCACCACCA 1163
              |||||||||||||||||||
Db   1 ACCACCACCACCACCACCA 16

RESULT 6
US-09-828-034-30
Sequence 30, Application US/09828034
Patent No. US20020064771A1
GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 30
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-30

Query Match   100.0%;   Pred. No. 6.6e+02;
Best Local Similarity   0.4%;   Score 16;   DB 10;   Length 21;
Matches 16;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1148 ACCACCACCACCACCACCA 1163
              |||||||||||||||||||
Db   3 ACCACCACCACCACCACCA 18

RESULT 7
US-09-828-034-31
Sequence 31, Application US/09828034
Patent No. US20020064771A1
GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 31
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-31

Query Match   100.0%;   Pred. No. 6.6e+02;
Best Local Similarity   0.4%;   Score 16;   DB 10;   Length 21;
Matches 16;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1148 ACCACCACCACCACCACCA 1163
              |||||||||||||||||||
Db   2 ACCACCACCACCACCACCA 17

RESULT 8
US-10-194-594-12/c
Sequence 12, Application US/10194594
Publication No. US20030044386A1
GENERAL INFORMATION:
; APPLICANT: Barber, Glen
; TITLE OF INVENTION: RECOMBINANT VSV FOR THE TREATMENT OF
; TITLE OF INVENTION: TUMOR CELLS
; FILE REFERENCE: 529372000200
; CURRENT APPLICATION NUMBER: US/10/194,594
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 60/304,125
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Vesicular stomatitis virus
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (2)..(12)
; OTHER INFORMATION: Polyadenylation/transcription stop signal of the
; OTHER INFORMATION: glycoprotein (G) gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(19)
; OTHER INFORMATION: Start sequence of the RNA polymerase L protein
US-10-194-594-12

Query Match   100.0%;   Pred. No. 6.6e+02;
Best Local Similarity   0.4%;   Score 16;   DB 9;   Length 22;
Matches 16;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1866 TTAGTTTTTTTCATAC 1881
              ||||||||||||||||
Db   16 TTAGTTTTTTTCATAC 1

RESULT 9
US-09-814-986-59
Sequence 59, Application US/09814986
Patent No. US20020068286A1
GENERAL INFORMATION:
; APPLICANT: Kleyn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/814,986
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/936,707
FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-814-986-59

Qy 1148 ACCACCACCACCACCA 1163
          ||||||||||||||||
Db   2   ACCACCACCACCACCA 17

RESULT 10
US-09-811-824-5/c
; Sequence 5, Application US/09811824
; Publication No. US20020182632A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, George P.
; APPLICANT: Mattoussi, Hedi
; APPLICANT: Mauro, J. Matthew
; APPLICANT: Bawendi, Moungi G.
; APPLICANT: Sundar, Vikram C.
; TITLE OF INVENTION: INORGANIC PARTICLE CONJUGATES
; FILE REFERENCE: 01997-282001
; CURRENT APPLICATION NUMBER: US/09/811,824
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,766
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-811-824-5

Query Match   0.4%; Score 16; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1148 ACCACCACCACCACCA 1163
          ||||||||||||||||
Db   21   ACCACCACCACCACCA 6

RESULT 11
US-09-045-620-3/c
; Sequence 3, Application US/09045620
; Patent No. US20010006793A1
; GENERAL INFORMATION:
; APPLICANT: BJORNSTI, Mary-Ann
; APPLICANT: HALL, David
; APPLICANT: KANG, Jason
; TITLE OF INVENTION: MODULATORS OF EUKARYOTIC CASPASES
; FILE REFERENCE: 209855.0027/27US
; CURRENT APPLICATION NUMBER: US/09/045,620
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplification primer
US-09-045-620-3

Query Match   0.4%; Score 16; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1148 ACCACCACCACCACCA 1163
          ||||||||||||||||
Db   29   ACCACCACCACCACCA 14

RESULT 12
US-09-728-466-19/c
; Sequence 19, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-728-466-19

Query Match   0.4%; Score 16; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1148 ACCACCACCACCACCA 1163
          ||||||||||||||||
Db   28   ACCACCACCACCACCA 13

RESULT 13
US-09-954-697-50/c
; Sequence 50, Application US/09954697

Patent No. US20020106631A1
GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
US-09-954-697-50
; SEQ ID NO 50
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer for small subunit of caspase-6

Query Match   0.4%;   Score 16;   DB 10;   Length 30;
Best Local Similarity   100.0%;   Pred. No. 6.9e+02;
Matches   16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1148   ACCACACCACCACCA   1163
            ||||||||||||||||
Db   28   ACCACACCACCACCA   13

RESULT 14
US-09-817-513A-22
; Sequence 22, Application US/09817513A
; Publication No. US20030044958A1
; GENERAL INFORMATION:
; APPLICANT: Staunton, Donald E.
; APPLICANT: Lipsky, Brian P.
; TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
; TITLE OF INVENTION: Binding/Signaling
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/817,513A
; FILING DATE: 28-Jun-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Young J. Suh
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/33886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-09-817-513A-22
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Query Match   0.4%;   Score 16;   DB 9;   Length 33;
Best Local Similarity   100.0%;   Pred. No. 6.9e+02;

Matches   16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1361   AGCTATGGAGGAGGAC   1376
            ||||||||||||||||
Db   9   AGCTATGGAGGAGGAC   24

RESULT 15
US-09-811-824-4
; Sequence 4, Application US/09811824
; Publication No. US20020182632A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, George P.
; APPLICANT: Mattoussi, Hedi
; APPLICANT: Mauro, J. Matthew
; APPLICANT: Bawendi, Moungi G.
; APPLICANT: Sundar, Vikram C.
; TITLE OF INVENTION: INORGANIC PARTICLE CONJUGATES
; FILE REFERENCE: 01997-282001
; CURRENT APPLICATION NUMBER: US/09/811,824
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,766
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
US-09-811-824-4
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer

Query Match   0.4%;   Score 16;   DB 9;   Length 34;
Best Local Similarity   100.0%;   Pred. No. 7e+02;
Matches   16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1148   ACCACACCACCACCA   1163
            ||||||||||||||||
Db   10   ACCACACCACCACCA   25

Search completed: March 14, 2003, 10:59:24
Job time : 249.857 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 04:35:16 ; Search time 5795.01 Seconds
           (without alignments)
           17068.215 Million cell updates/sec

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccagtaaggagtcggggtc..........aaatcttttattcaaataaa 3934

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size :   0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :   Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US095_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US06001_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US06002_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US06003_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US06004_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US06005_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US06006_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US06007_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US06008_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US06009_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US06010_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US06011_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US06012_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US06013_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US06014_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US06015_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US06016_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US06017_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US06018_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US06019_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US06020_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US06021_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US06022_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US06023_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US06024_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US06025_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US06026_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US06027_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US06028_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US06029_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US06030_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US06031_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US06032_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US06033_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US06034_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US06035_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US06036_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US06037_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US06038_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US06039_COMB.seq:*
84: /cgn2_6/ptodata/1/pna/US06040_COMB.seq:*
85: /cgn2_6/ptodata/1/pna/US06041_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	46	1.2	46	8	US-08-472-801-2244 Sequence 2244, Ap
2	46	1.2	46	10	US-08-668-235-2244 Sequence 2244, Ap
3	42	1.1	42	8	US-08-472-801-2235 Sequence 2235, Ap
4	42	1.1	42	10	US-08-668-235-2235 Sequence 2235, Ap
5	40	1.0	40	8	US-08-472-801-2249 Sequence 2249, Ap
6	40	1.0	40	10	US-08-668-235-2249 Sequence 2249, Ap
7	35	0.9	35	8	US-08-472-801-2258 Sequence 2258, Ap
8	35	0.9	35	10	US-08-668-235-2258 Sequence 2258, Ap
9	35	0.9	35	8	US-08-472-801-2262 Sequence 2262, Ap
10	35	0.9	35	10	US-08-668-235-2262 Sequence 2262, Ap
11	34	0.9	34	8	US-08-472-801-2233 Sequence 2233, Ap
12	34	0.9	34	10	US-08-668-235-2233 Sequence 2233, Ap
13	34	0.9	34	8	US-08-472-801-2239 Sequence 2239, Ap
14	34	0.9	34	10	US-08-668-235-2239 Sequence 2239, Ap
15	34	0.9	34	8	US-08-472-801-2242 Sequence 2242, Ap
16	34	0.9	34	10	US-08-668-235-2242 Sequence 2242, Ap
17	32	0.8	32	8	US-08-472-801-2252 Sequence 2252, Ap
18	32	0.8	32	10	US-08-668-235-2252 Sequence 2252, Ap
19	31	0.8	31	8	US-08-472-801-2231 Sequence 2231, Ap
20	31	0.8	31	10	US-08-668-235-2231 Sequence 2231, Ap
21	31	0.8	31	8	US-08-472-801-2247 Sequence 2247, Ap

c	22	31	0.8	10	US-08-668-235-2231	Sequence 2231, Ap
c	23	31	0.8	10	US-08-668-235-2247	Sequence 2247, Ap
c	24	31	0.8	10	US-08-668-235-2255	Sequence 2255, Ap
c	25	30	0.8	1	PCT-US00-00969-19	Sequence 19, Appl
c	26	30	0.8	18	US-09-483-104-19	Sequence 19, Appl
c	27	30	0.8	10	US-08-472-801-2234	Sequence 2234, Ap
c	28	24	0.6	8	US-08-472-801-2254	Sequence 2254, Ap
c	29	24	0.6	10	US-08-668-235-2234	Sequence 2234, Ap
c	30	24	0.6	10	US-08-668-235-2254	Sequence 2254, Ap
c	31	23	0.6	10	US-08-668-235-2236	Sequence 2236, Ap
c	32	23	0.6	8	US-08-472-801-2236	Sequence 2236, Ap
c	33	23	0.6	8	US-08-472-801-2240	Sequence 2240, Ap
c	34	23	0.6	8	US-08-472-801-2248	Sequence 2248, Ap
c	35	23	0.6	8	US-08-472-801-2250	Sequence 2250, Ap
c	36	23	0.6	8	US-08-472-801-2251	Sequence 2251, Ap
c	37	23	0.6	8	US-08-472-801-2253	Sequence 2253, Ap
c	38	23	0.6	8	US-08-472-801-2259	Sequence 2259, Ap
c	39	23	0.6	10	US-08-668-235-2236	Sequence 2236, Ap
c	40	23	0.6	10	US-08-668-235-2240	Sequence 2240, Ap
c	41	23	0.6	10	US-08-668-235-2248	Sequence 2248, Ap
c	42	23	0.6	10	US-08-668-235-2250	Sequence 2250, Ap
c	43	23	0.6	10	US-08-668-235-2251	Sequence 2251, Ap
c	44	23	0.6	10	US-08-668-235-2253	Sequence 2253, Ap
c	45	23	0.6	38	US-08-668-235-2259	Sequence 2259, Appli

RESULT 1
US-08-472-801-2244/c
Sequence 2244, Application US/08472801
GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2244
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2244

ALIGNMENTS

Qy   534 GTCACTACCCTCGACGCCCGCCGCCAGCGAGAGGAGGAGGAGGACGAG 579
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   46 GTCACTACCCTCGACGCCCGCCGCCAGCGAGAGGAGGAGGAGGACGAG 1

Query Match   1.2%;   Score 46;   DB 8;   Length 46;
Best Local Similarity 100.0%;   Pred. No. 8.6e-11;
Matches 46;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2244
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2244

Qy   534 GTCACTACCCTCGACGCCCGCCGCCAGCGAGAGGAGGAGGAGGACGAG 579
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   46 GTCACTACCCTCGACGCCCGCCGCCAGCGAGAGGAGGAGGAGGACGAG 1

Query Match   1.2%;   Score 46;   DB 10;   Length 46;
Best Local Similarity 100.0%;   Pred. No. 8.6e-11;
Matches 46;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
US-08-472-801-2244

RESULT 3
US-08-472-801-2235/c
Sequence 2235, Application US/08472801
GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2235
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2235

Qy   192 CCGGCGAGAGATAGGGGAGGGGAGGGGAGGCCGGCCGCCGGGTGATTGG 233
          ||||||||||||||||||||||||||||||||||||||||||||
Db   42 CCGGCGAGAGATAGGGGAGGGGAGGGGAGGCCGGCCGCCGGGTGATTGG 1

Query Match   1.1%;   Score 42;   DB 8;   Length 42;
Best Local Similarity 100.0%;   Pred. No. 8e-09;
Matches 42;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

RESULT 4
US-08-668-235-2235/c
Sequence 2235, Application US/08668235
GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2235
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2235

Query Match   1.1%;   Score 42;   DB 10;   Length 42;
Best Local Similarity 100.0%;   Pred. No. 8e-09;
Matches 42;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

RESULT 2
US-08-668-235-2244/c
Sequence 2244, Application US/08668235
GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; SEQ ID NO 2244
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2244

Qy   534 GTCACTACCCTCGACGCCCGCCGCCAGCGAGAGGAGGAGGAGGACGAG 579
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   46 GTCACTACCCTCGACGCCCGCCGCCAGCGAGAGGAGGAGGAGGACGAG 1

Query Match   1.2%;   Score 46;   DB 10;   Length 46;
Best Local Similarity 100.0%;
Matches 46;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy    192 CCGGCGAGAGAGATAGGGGAGGGAGGGAGGCCGGCCGGCCGGGTGATTGG 233
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db     42 CCGGCGAGAGATAGGGGAGGGAGGGAGGCCGGCCGGCCGGGTGATTGG 1
```

RESULT 5
US-08-472-801-2249/c
Sequence 2249, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Smith, Larry J.
; APPLICANT: Hesed 2
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprogramming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2249
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2249

Query Match   1.0%; Score 40; DB 8; Length 40;
Best Local Similarity   100.0%; Pred. No. 7.7e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   3215 GGAAGAACTGCCTGCCTGCCCATCTCAGAGCCATAAGGT 3254
          |||||||||||||||||||||||||||||||||||||||
Db     40 GGAAGAACTGCCTGCCTGCCCATCTCAGAGCCATAAGGT 1
```

RESULT 6
US-08-668-235-2249/c
Sequence 2249, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; APPLICANT: Hesed-1
; TITLE OF INVENTION: Methods and Compositions for Cellular
; TITLE OF INVENTION: Reprogramming
; FILE REFERENCE: Hesed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2249
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2249

Query Match   1.0%; Score 40; DB 10; Length 40;
Best Local Similarity   100.0%; Pred. No. 7.7e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   3215 GGAAGAACTGCCTGCCTGCCCATCTCAGAGCCATAAGGT 3254
          |||||||||||||||||||||||||||||||||||||||
Db     40 GGAAGAACTGCCTGCCTGCCCATCTCAGAGCCATAAGGT 1
```

RESULT 7
US-08-472-801-2258/c
Sequence 2258, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprogramming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2258
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2258

RESULT 8
US-08-472-801-2262/c
Sequence 2262, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprogramming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2262
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2262

Query Match   0.9%; Score 35; DB 8; Length 35;
Best Local Similarity   100.0%; Pred. No. 2.2e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    403 GCCGCTGAGCGCCATCACGTCGCCCGAAGAGGAGCT 437
          ||||||||||||||||||||||||||||||||||||
Db     35 GCCGCTGAGCGCCATCACGTCGCCCGAAGAGGAGCT 1
```

RESULT 9
US-08-668-235-2258/c
Sequence 2258, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; APPLICANT: Hesed-1
; TITLE OF INVENTION: Methods and Compositions for Cellular
; TITLE OF INVENTION: Reprogramming
; FILE REFERENCE: Hesed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2258
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2258

Query Match   0.9%; Score 35; DB 8; Length 35;
Best Local Similarity   100.0%; Pred. No. 2.2e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    628 GCCACCGGCGCCAAGGACACAAAGCCAATGGGCAG 662
          |||||||||||||||||||||||||||||||||||
Db     35 GCCACCGGCGCCAAGGACACAAAGCCAATGGGCAG 1
```

RESULT 10
US-08-668-235-2262/c
; Sequence 2262, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2262
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2262

Query Match   0.9%; Score 35; DB 10; Length 35;
Best Local Similarity   100.0%; Pred. No. 2.2e-05;
Matches   35; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   403 GCCGGCTGACGCCCATCATGTCGCCCGGAAGAGGAGCT 437
          ||||||||||||||||||||||||||||||||||||
Db   35 GCCGGCTGACGCCCATCATGTCGCCCGGAAGAGGAGCT 1

RESULT 11
US-08-472-801-2233/c
; Sequence 2233, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2233
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2233

Query Match   0.9%; Score 35; DB 10; Length 35;
Best Local Similarity   100.0%; Pred. No. 2.2e-05;
Matches   35; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   628 GCCACCCGGCGCCAAGGACGACACAAAGCCAATGGGCAG 662
          |||||||||||||||||||||||||||||||||||
Db   35 GCCACCCGGCGCCAAGGACGACACAAAGCCAATGGGCAG 1

RESULT 12
US-08-472-801-2239/c
; Sequence 2239, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2239
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2239

Query Match   0.9%; Score 34; DB 8; Length 34;
Best Local Similarity   100.0%; Pred. No. 6.9e-05;
Matches   34; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   150 CCCGGGGAGGCCGACTTTTGGCTACGGAGAGGAG 183
          ||||||||||||||||||||||||||||||||||
Db   34 CCCGGGGAGGCCGACTTTTGGCTACGGAGAGGAG 1

RESULT 13
US-08-472-801-2242/c
; Sequence 2242, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2242
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2242

Query Match   0.9%; Score 34; DB 8; Length 34;
Best Local Similarity   100.0%; Pred. No. 6.9e-05;
Matches   34; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   260 CCACCCTCACGCCAGACTCCCGGAGGGTCGCGCG 293
          ||||||||||||||||||||||||||||||||||
Db   34 CCACCCTCACGCCAGACTCCCGGAGGGTCGCGCG 1

RESULT 14
US-08-668-235-2233/c
; Sequence 2233, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Hesed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Methods and Compositions for Cellular
; TITLE OF INVENTION: Reprograming
; FILE REFERENCE: Hesed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2233
; LENGTH: 34

Query Match   0.9%; Score 34; DB 8; Length 34;
Best Local Similarity   100.0%; Pred. No. 6.9e-05;
Matches   34; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   485 CGCTGCTCGGAGTTGGTCGGGGGAAGTCTGGTAATAA 518
          |||||||||||||||||||||||||||||||||||
Db   34 CGCTGCTCGGAGTTGGTCGGGGGAAATCTGGTAATAA 1

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-668-235-2233

Query Match       0.9%;    Score 34;  DB 10;  Length 34;
Best Local Similarity   100.0%;  Pred. No. 6.9e-05;
Matches  34;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   150 CCCGGGAGGGCGGACTTTTGGCTACGGAGAAGGAG 183
         ||||||||||||||||||||||||||||||||||
Db    34 CCCGGGAGGGCCGACTTTTGGCTACGGAGAAGGAG 1

RESULT 15
US-08-668-235-2239/c
;  Sequence 2239, Application US/08668235
;  GENERAL INFORMATION:
;  APPLICANT: Larry J.      Smith
;  TITLE OF INVENTION: Methods and Compositions for Cellular
;  TITLE OF INVENTION: Reprogramming
;  FILE REFERENCE: Hesed-1
;  CURRENT APPLICATION NUMBER: US/08/668,235
;  CURRENT FILING DATE: 1996-06-17
;  EARLIER APPLICATION NUMBER: 07/748,997
;  EARLIER FILING DATE: 08/23/91
;  EARLIER APPLICATION NUMBER: 08/426,781
;  EARLIER FILING DATE: 04/22/95
;  EARLIER APPLICATION NUMBER: 08/472,801
;  EARLIER FILING DATE: 06/07/95
;  NUMBER OF SEQ ID NOS: 3629
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 2239
;  LENGTH: 34
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-08-668-235-2239

Query Match       0.9%;    Score 34;  DB 10;  Length 34;
Best Local Similarity   100.0%;  Pred. No. 6.9e-05;
Matches  34;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   260 CCACCCTCACGCCCAGAGACTCCCGGAGGGTCGCGCG 293
         |||||||||||||||||||||||||||||||||||
Db    34 CCACCCTCACGCCCAGAGACTCCCGGAGGGTCGCGCG 1

Search completed: March 14, 2003, 10:28:01
Job time : 5797.01 secs
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: March 14, 2003, 04:47:29 ; Search time 1076.55 seconds
(without alignments)
8302.956 Million cell updates/sec

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccagtaaggagtcggggtc.........aaatctttattcaaataa 3934

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4666902 seqs, 1136064160 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7027196

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	25	0.6	25	8	US-10-236-392-256	Sequence 256, App
c	2	24	0.6	24	8	US-10-293-338-8053	Sequence 8053, Ap
c	3	24	0.6	24	8	US-10-310-188-79749	Sequence 79749, A
c	4	23	0.6	25	9	US-60-427-836-454577	Sequence 454577,
c	5	22	0.6	22	8	US-10-310-188-2068	Sequence 2068, Ap
c	6	21	0.5	21	8	US-60-427-808-7862	Sequence 7862, Ap
c	7	21	0.5	21	8	US-10-310-188-73447	Sequence 73447, A
c	8	21	0.5	25	8	US-10-355-577-900097	Sequence 900097,
c	9	20	0.5	20	8	US-10-293-338-3254	Sequence 3254, Ap
c	10	20	0.5	20	8	US-10-310-188-81944	Sequence 81944, A
c	11	20	0.5	20	8	US-10-169-983-57	Sequence 57, Appl
c	12	20	0.5	20	8	US-10-169-983-58	Sequence 58, Appl
c	13	20	0.5	25	8	US-10-293-338-23817	Sequence 23817, A
c	14	20	0.5	19	8	US-10-310-188-12275	Sequence 1275, App
c	15	19	0.5	19	8	US-10-310-188-57069	Sequence 57069, A
c	16	19	0.5	19	8	US-10-310-188-68525	Sequence 68525, A
c	17	19	0.5	25	9	US-60-427-808-56931	Sequence 56931, A
c	18	19	0.5	18	8	US-10-303-778-1607	Sequence 1607, Ap
c	19	19	0.5	18	8	US-10-303-778-8650	Sequence 8650, Ap
c	20	19	0.5	18	8	US-10-310-188-744	Sequence 744, App
c	21	18	0.5	18	8	US-10-310-188-79750	Sequence 79750, A
c	22	18	0.5	25	9	US-60-427-808-541112	Sequence 541112,
c	23	18	0.5	25	9	US-60-427-836-102497	Sequence 102497,
c	24	18	0.5	25	9	US-60-427-836-237621	Sequence 237621,
c	25	18	0.5	25	9	US-60-427-836-571386	Sequence 571386,
c	26	18	0.5	41	9	US-60-449-155-609	Sequence 609, App
c	27	17	0.5	17	8	US-10-303-778-16089	Sequence 16089, A
c	28	17	0.4	17	8	US-10-310-188-31362	Sequence 31362, A
c	29	17	0.4	17	8	US-10-236-392-255	Sequence 255, App
c	30	17	0.4	18	8	US-10-310-188-79759	Sequence 79759, A
c	31	17	0.4	20	8	US-10-310-188-48654	Sequence 48654, A
c	32	17	0.4	21	8	US-10-310-188-29017	Sequence 29017, A
c	33	17	0.4	21	8	US-10-310-188-62082	Sequence 62082, A
c	34	17	0.4	25	8	US-10-355-577-7439	Sequence 7439, Ap
c	35	17	0.4	25	8	US-10-355-577-106353	Sequence 106353,
c	36	17	0.4	25	8	US-10-355-577-476248	Sequence 476248,
c	37	17	0.4	25	8	US-10-355-577-870929	Sequence 870929,
c	38	17	0.4	25	8	US-60-427-808-136571	Sequence 136571,
c	39	17	0.4	25	9	US-60-427-808-179014	Sequence 179014,
c	40	17	0.4	25	9	US-60-427-808-409599	Sequence 409599,
c	41	17	0.4	25	9	US-60-427-836-65488	Sequence 65488, A
c	42	17	0.4	25	9	US-60-427-836-321372	Sequence 321372,
c	43	17	0.4	32	7	US-10-287-787-13609	Sequence 13609, A
c	44	17	0.4	42	8	US-10-050-902-297	Sequence 297, App
c	45	17	0.4	42	8	US-10-050-902-298	Sequence 298, App

ALIGNMENTS

RESULT 1
US-10-236-392-256/c
; Sequence 256, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine L
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Ediger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303

```
;   PRIOR FILING DATE: 2002-02-15
;   PRIOR APPLICATION NUMBER: US60/367,753
;   PRIOR FILING DATE: 2002-03-25
;   PRIOR APPLICATION NUMBER: US60/369,479
;   PRIOR FILING DATE: 2002-04-02
;   PRIOR APPLICATION NUMBER: US09/659,634
;   PRIOR FILING DATE: 2000-09-12
;   PRIOR APPLICATION NUMBER: US60/318,120
;   PRIOR FILING DATE: 2001-09-07
;   PRIOR APPLICATION NUMBER: US60/318,130
;   PRIOR FILING DATE: 2001-09-07
;   PRIOR APPLICATION NUMBER: US60/392-256
;   PRIOR FILING DATE: 2001-09-07
;   OTHER INFORMATION: Description of Artificial Sequence: probe
;   FEATURE:
;   ORGANISM: Artificial Sequence
;   TYPE: DNA
;   LENGTH: 25
;   SEQ ID NO 256
;   SOFTWARE: Custom
;   NUMBER OF SEQ ID NOS: 794
; Remaining Prior Application data removed - See File Wrapper or PALM.

Qy          678 CAGGAAGGCGGCTGGAGAGACCTTACGA 702
                ||||||||||||||||||||||||||||
Db           25 CAGGAAGGCGGCTGGAGAGACCTTACGA 1

Query Match             0.6%;  Score 25;  DB 8;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 0.079;
Matches  25;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 2
US-10-293-338-8053/c
; Sequence 8053, Application US/10293338
; GENERAL INFORMATION:
;   APPLICANT: RosettaGenomics LTD
;   TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
    TITLE OF INVENTION: THEREOF
;   CURRENT APPLICATION NUMBER: US/10/293,338
;   CURRENT FILING DATE: 2002-11-14
;   FILE REFERENCE: 45282
;   NUMBER OF SEQ ID NOS: 8785
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 8053
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-293-338-8053

Qy         1330 AGTTTCAGCAACAAACAAAACTTTG 1353
                ||||||||||||||||||||||||
Db           24 AGTTTCAGCAACAAACAAAACTTTG 1

Query Match             0.6%;  Score 24;  DB 8;  Length 24;
Best Local Similarity  100.0%;  Pred. No. 0.26;
Matches  24;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 3
US-10-310-188-79749/c
; Sequence 79749, Application US/10310188
; GENERAL INFORMATION:
;   APPLICANT: RosettaGemonics
;   TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 47487
;   CURRENT APPLICATION NUMBER: US/10/310,188
;   CURRENT FILING DATE: 2002-12-19
;   NUMBER OF SEQ ID NOS: 86841
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 79749
;   LENGTH: 24
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-10-310-188-79749

Qy         1146 CAACCACCACCACCACCACCAAAACCA 1169
                |||||||||||||||||||||||||||
Db           24 CAACCACCACCACCACCACCAAAACCA 1

Query Match             0.6%;  Score 24;  DB 8;  Length 24;
Best Local Similarity  100.0%;  Pred. No. 0.26;
Matches  24;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 4
US-60-427-836-454577
; Sequence 454577, Application US/60427836
; GENERAL INFORMATION:
;   APPLICANT: Xue Mei Zhou
;   TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;   FILE REFERENCE: 3527
;   CURRENT APPLICATION NUMBER: US/60/427,836
;   CURRENT FILING DATE: 2002-11-20
;   NUMBER OF SEQ ID NOS: 699466
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;   SEQ ID NO 454577
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-454577

Qy          748 GGCATGCTTCGGAAACTGGACAT 770
                |||||||||||||||||||||||
Db            2 GGCATGCTTCGGAAACTGGACAT 24

Query Match             0.6%;  Score 23;  DB 9;  Length 25;
Best Local Similarity  100.0%;  Pred. No. 0.84;
Matches  23;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 5
US-10-310-188-2068/c
; Sequence 2068, Application US/10310188
; GENERAL INFORMATION:
;   APPLICANT: RosettaGemonics
;   TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 47487
;   CURRENT APPLICATION NUMBER: US/10/310,188
;   CURRENT FILING DATE: 2002-12-19
;   NUMBER OF SEQ ID NOS: 86841
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 2068
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-310-188-2068

Qy         2430 GCAGGCTAGTCTAACCATGGTG 2451
                ||||||||||||||||||||||
Db           22 GCAGGCTAGTCTAACCATGGTG 1

Query Match             0.6%;  Score 22;  DB 8;  Length 22;
Best Local Similarity  100.0%;  Pred. No. 2.7;
Matches  22;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 6
US-10-310-188-7862/c
; Sequence 7862, Application US/10310188
; GENERAL INFORMATION:
;   APPLICANT: RosettaGemonics
;   TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 47487
```

CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 7862
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-7862

Query Match   100.0%; Score 21; DB 8; Length 21;
Best Local Similarity   100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3541 ACACCCCAAGTGGTTTGGGAA 3561
        |||||||||||||||||||||
Db   21 ACACCCCAAGTGGTTTGGGAA 1

RESULT 7
US-10-310-188-73447/c
Sequence 73447, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 73447
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-73447

Query Match   100.0%; Score 21; DB 8; Length 21;
Best Local Similarity   100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1211 CACCCTAGCAACCTAGCCAGA 1231
        |||||||||||||||||||||
Db   21 CACCCTAGCAACCTAGCCAGA 1

RESULT 8
US-10-355-577-900097
Sequence 900097, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 900097
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-900097

Query Match   0.5%; Score 21; DB 8; Length 25;
Best Local Similarity   100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3578 GGGTTTATAGGGGAGGAGGAG 3598
        |||||||||||||||||||||
Db   5 GGGTTTATAGGGGAGGAGGAG 25

RESULT 9

US-10-293-338-3254/c
Sequence 3254, Application US/10293338
GENERAL INFORMATION:
APPLICANT: RosettaGenomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES ?
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: Patentin version 3.1
SEQ ID NO 3254
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-3254

Query Match   0.5%; Score 20; DB 8; Length 20;
Best Local Similarity   100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1308 CTGTCTGAAAGAAGCAAAGT 1327
        ||||||||||||||||||||
Db   20 CTGTCTGAAAGAAGCAAAGT 1

RESULT 10
US-10-310-188-81944/c
Sequence 81944, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILE REFERENCE: 47487
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 81944
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-81944

Query Match   0.5%; Score 20; DB 8; Length 20;
Best Local Similarity   100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2636 TGAAATTGCTGATTGTTCTG 2655
        ||||||||||||||||||||
Db   20 TGAAATTGCTGATTGTTCTG 1

RESULT 11
US-10-169-983-57
Sequence 57, Application US/10169983
GENERAL INFORMATION:
APPLICANT: Takara Shuzo Co., Ltd.
TITLE OF INVENTION: Therapeutic agents
FILE REFERENCE: 01-011-PCT
CURRENT APPLICATION NUMBER: US/10/169,983
CURRENT FILING DATE: 2002-07-14
PRIOR APPLICATION NUMBER: JP 2000-4989
PRIOR APPLICATION FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: JP 2000-303711
PRIOR APPLICATION FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed primer based on nucleotide sequence of

RESULT 12
US-10-169-983-57
; OTHER INFORMATION: human myeloid leukemia cell differentiation protein-1 mRNA.

Qy 749 GCATGCTTCGGAAACTGGAC 768
        ||||||||||||||||||||
Db   1 GCATGCTTCGGAAACTGGAC 20

Query Match   100.0%; Score 20; DB 8; Length 20;
Best Local Similarity   100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
US-10-169-983-58/c
; Sequence 58, Application US/10169983
; GENERAL INFORMATION:
; APPLICANT: Takara Shuzo Co., Ltd.
; TITLE OF INVENTION: Therapeutic agents
; FILE REFERENCE: 01-011-PCT
; CURRENT APPLICATION NUMBER: US/10/169,983
; CURRENT FILING DATE: 2002-07-14
; PRIOR APPLICATION NUMBER: JP 2000-4989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: JP 2000-303711
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed primer based on nucleotide sequence of
; OTHER INFORMATION: human myeloid leukemia cell differentiation protein-1 mRNA.
US-10-169-983-58

Qy 1182 GGACTCCAAGCTGTAACTTC 1201
        ||||||||||||||||||||
Db   20 GGACTCCAAGCTGTAACTTC 1

Query Match   100.0%; Score 20; DB 8; Length 20;
Best Local Similarity   100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-60-427-808-23817
; Sequence 23817, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23817
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-23817

Qy 1048 AATGTGCTGCTGGGCTTTTGC 1067
        |||||||||||||||||||||
Db   2 AATGTGCTGCTGGGCTTTTGC 21

Query Match   100.0%; Score 20; DB 9; Length 25;
Best Local Similarity   100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-10-293-338-1275/c
; Sequence 1275, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES A
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1275
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-1275

Qy 1772 ATTCTTAAGACAGCTTGTA 1790
        |||||||||||||||||||
Db   19 ATTCTTAAGACAGCTTGTA 1

Query Match   100.0%; Score 19; DB 8; Length 19;
Best Local Similarity   100.0%;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
US-10-310-188-57069/c
; Sequence 57069, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57069
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-57069

Qy 1133 GTTGACTTTTAACCAACCA 1151
        |||||||||||||||||||
Db   19 GTTGACTTTTAACCAACCA 1

Query Match   100.0%; Score 19; DB 8; Length 19;
Best Local Similarity   100.0%;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: March 14, 2003, 10:49:54
Job time : 1078.55 secs

OM nucleic - nucleic search, using sw model

```
                    GenCore version 5.1.4_p5_4578
                    Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:             March 14, 2003, 04:32:49 ; Search time 3692.82 Seconds
                                                (without alignments)
                                                17253.226 Million cell updates/sec

Title:              US-09-869-894-18
Perfect score:      3934
Sequence:           1 tccagtaaggagtcggggtc.........aaatctttattcaaataaa 3934

Scoring table:      OLIGO_NUC
                    Gapop 60.0 , Gapext 60.0

Searched:           16154066 seqs, 8097743376 residues

Word size :         0

Total number of hits satisfying chosen parameters:       102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :          EST:*
                    1: em_estba:*
                    2: em_esthum:*
                    3: em_estin:*
                    4: em_estmu:*
                    5: em_estov:*
                    6: em_estpl:*
                    7: em_estro:*
                    8: em_htc:*
                    9: em_htc1:*
                   10: gb_est1:*
                   11: gb_est2:*
                   12: gb_est3:*
                   13: gb_est4:*
                   14: gb_est5:*
                   15: em_estfun:*
                   16: em_estom:*
                   17: gb_gss:*
                   18: em_gss_hum:*
                   19: em_gss_inv:*
                   20: em_gss_pln:*
                   21: em_gss_vrt:*
                   22: em_gss_fun:*
                   23: em_gss_mam:*
                   24: em_gss_mus:*
                   25: em_gss_Other:*
                   26: em_gss_pro:*
                   27: em_gss_rod:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	0.8	31	9	AA463890	AA463890 aa08d03.s
2	23	0.6	26	17	A2365602	A2365602 1M012017
3	21	0.5	34	17	A2343185	A2343185 1M0076C22
4	21	0.5	49	9	AI569150	AI569150 tr83a03.x
5	18	0.5	35	17	A2304663	A2304663 1M0004016
6	18	0.5	44	17	A2453451	A2453451 1M0254P10

```
c  7  17  0.4  28  17  A2403083  A2403083 1M0170P09
c  8  17  0.4  40  14  H28644    H28644 y152h05.r1
c  9  17  0.4  43  17  A2637149  A2637149 1M0496F19
c 10  17  0.4  19  17  A2315293  A2315293 1M0032P20
c 11  16  0.4  20  17  A2622226  A2622226 1M0455A24
c 12  16  0.4  23  17  A2784648  A2784648 2M0027P11
c 13  16  0.4  23  17  A2860972  A2860972 2M0167A16
c 14  16  0.4  24  17  A2449706  A2449706 2M0248M02
c 15  16  0.4  26  17  A2405428  A2405428 1M0174D13
c 16  16  0.4  28  17  A2512393  A2512393 1M0357F20
c 17  16  0.4  28  17  A2947343  A2947343 2M0210G06
c 18  16  0.4  30  17  A2821583  A2821583 2M0094123
c 19  16  0.4  33  17  A2401045  A2401045 1M0167P03
c 20  16  0.4  33  17  A2829628  A2829628 2M0107105
c 21  16  0.4  36  17  A2346286  A2346286 1M0081C01
c 22  16  0.4  37  17  TA35D05P  TA35D05P
c 23  16  0.4  41  17  A2662472  A2662472 1M0541A09
c 24  16  0.4  42  17  A2632020  A2632020 1M0486P23
c 25  16  0.4  45  17  A2602225  A2602225 1M0420F20
c 26  16  0.4  46  17  A2993993  A2993993 2M0279E13
c 27  16  0.4  48  17  A2489134  A2489134 1M0319H14
c 28  16  0.4  50  17  A2657819  A2657819 1M0534E17
c 29  16  0.4  50  17  A2964472  A2964472 2M0234J11
c 30  15  0.4  25  13  BG927349  BG927349 HNC1-1-C4
c 31  15  0.4  26  17  A2479681  A2479681 1M0300G02
c 32  15  0.4  32  17  A2792853  A2792853 2M0045C07
c 33  15  0.4  33  10  AW698829  AW698829 r436 non-
c 34  15  0.4  34  17  A2936680  A2936680 2M0193D01
c 35  15  0.4  35  17  A2999984  A2999984 2M0287M03
c 36  15  0.4  37  17  A2392980  A2392980 1M0155P13
c 37  15  0.4  37  17  BH863503  BH863503 SALK_0940
c 38  15  0.4  40  17  A2788014  A2788014 2M0034A21
c 39  15  0.4  41  17  A2390426  A2390426 1M0151117
c 40  15  0.4  43  9   AA209184  AA209184 zg85c06.r
c 41  15  0.4  48  17  A2300919  A2300919 EP(2)0882
c 42  15  0.4  50  9   AU102484  AU102484 AU102484
c 43  15  0.4  50  9   AU103585  AU103585 AU103585
c 44  15  0.4  50  9   AU106893  AU106893 AU106893
c 45  15  0.4  50  9   AU106894  AU106894 AU106894
```

ALIGNMENTS

```
RESULT 1
AA463890
LOCUS       AA463890                 31 bp     mRNA      linear     EST 10-JUN-1997
DEFINITION  aa08d03.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:812645 3',
            similar to SW:MCL1_HUMAN Q07820 INDUCED MYELOID LEUKEMIA CELL
            DIFFERENTIATION PROTEIN MCL1. ;, mRNA sequence.
ACCESSION   AA463890
VERSION     AA463890.1    GI:2188774
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
AUTHORS     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            , T., Waterston,R. and Wilson,R.
TITLE       Washu-Merck EST Project 1997
JOURNAL     Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
```

Seq primer: -4ln13 fwd, ET from Amersham
High quality sequence stop: 19.

```
FEATURES
     source          1..31
                     /organism="Homo sapiens"
                     /db_xref="GDB:6043555"
                     /db_xref="taxon:9606"
                     /clone=IMAGE:812645"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
```

BASE COUNT   6 a   9 c   13 g   3 t
ORIGIN

Qy   375 GGCGGCCGCTTGAGGAGAGATGGAAGCCCCGGC 404
         |||||||||||||||||||||||||||||||||
Db   1 GGCGGCCGCTTGAGGAGAGATGGAAGCCCCGGC 30

RESULT 2
AZ355602/c
LOCUS   AZ355602   26 bp   DNA   linear   GSS 02-OCT-2000
DEFINITION 1M0112017F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0112017 F, DNA sequence.
ACCESSION   AZ355602
VERSION   AZ355602.1 GI:10479302
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0112   row: O   column: 17
            Seq primer: CGTGTGTAAAACAGCGACCAGT
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES
     source   1..26
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
```

Query Match    0.8%;   Score 30;   DB 9;   Length 31;
Best Local Similarity   100.0%;   Pred. No. 0.0029;
Matches 30;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   375 GGCGGCCGCTTGAGGAGAGATGGAAGCCCCGGC 404
         |||||||||||||||||||||||||||||||||
Db     1 GGCGGCCGCTTGAGGAGAGATGGAAGCCCCGGC 30

---

RESULT 3
AZ343185/c
LOCUS       AZ343185              34 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0076022R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0076C22 R, DNA sequence.
ACCESSION   AZ343185
VERSION     AZ343185.1  GI:10421362
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076   row: C   column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES
     source          1..34
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0112017"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|14732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

BASE COUNT   0 a   1 c   14 g   11 t
ORIGIN

Query Match   0.6%;   Score 23;   DB 17;   Length 26;
Best Local Similarity   100.0%;   Pred. No. 9.9;
Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1148 ACCACCACCACCACCAAAACCAG 1170
         |||||||||||||||||||||||
Db   23 ACCACCACCACCACCAAAACCAG 1

RESULT 4
AI569150/c

LOCUS   AI569150   49 bp   mRNA   linear   EST 29-MAR-1999
DEFINITION t83a03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224876 3',
            mRNA sequence.
ACCESSION   AI569150
VERSION   AI569150.1 GI:4532524
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ctgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.

FEATURES   Location/Qualifiers
     source   1..49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NCI_CGAP_Pan1"
                     /clone="IMAGE:2224876"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT;
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"

BASE COUNT   18 a   7 c   2 g   22 t

ORIGIN

Qy 1148 ACCACCACCACCACAAAACC 1168
         ||||||||||||||||||||
Db   23 ACCACCACCACCACAAAACC 3

Query Match   0.5%; Score 21; DB 17; Length 34;
Best Local Similarity   100.0%;   Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 ACCACCACCACCACAAAACC 1168
         ||||||||||||||||||||
Db   23 ACCACCACCACCACAAAACC 3

RESULT 5
AZ304663/c

LOCUS   AZ304663   35 bp   DNA   linear   GSS 29-SEP-2000
DEFINITION 1M0004016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0004016 R, DNA sequence.
ACCESSION   AZ304663
VERSION   AZ304663.1 GI:10340903
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 35)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0004   row: O   column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 35.

FEATURES   Location/Qualifiers
     source   1..35
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0004016"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD4nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|47321114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid RI. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

BASE COUNT   2 a   2 c   18 g   13 t

ORIGIN

Qy 1797 TTTGTAAAAATTGTATATA 1815
         ||||||||||||||||||||
Db   41 TTTGTAAAAATTGTATATA 23

Query Match   0.5%; Score 19; DB 9; Length 49;
Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1797 TTTGTAAAAATTGTATATA 1815
         ||||||||||||||||||||
Db   41 TTTGTAAAAATTGTATATA 23

RESULT 6
AZ453451/c

ORIGIN

Qy   1148 ACCACCACCACCACCAAA 1165
             |||||||||||||||||||
Db   26 ACCACCACCACCACCAA 9

Query Match   0.5%;   Score 18;   DB 17;   Length 35;
Best Local Similarity   100.0%;   Pred. No. 3.1e+03;
Matches 18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

LOCUS   AZ453451   44 bp   DNA   linear   GSS 04-OCT-2000
DEFINITION   1M0254P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0254P10 R, DNA sequence.
ACCESSION   AZ453451
VERSION   AZ453451.1   GI:10611092
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 44)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
             ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000   Std Error: 0.00
             Plate: 0254 row: P column: 10
             Seq primer: CACACAGGAAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 44.
FEATURES   Location/Qualifiers
     source   1..44
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0254P10"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|14732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

BASE COUNT   2 a   2 c   15 g   25 t

RESULT 7
AZ403083/c

ORIGIN

Qy   1147 AACCACCACCACCACCAA 1164
             |||||||||||||||||||
Db   38 AACCACCACCACCACCAA 21

Query Match   0.5%;   Score 18;   DB 17;   Length 44;
Best Local Similarity   100.0%;   Pred. No. 3.1e+03;
Matches 18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

LOCUS   AZ403083   28 bp   DNA   linear   GSS 03-OCT-2000
DEFINITION   1M0170P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0170P09 R, DNA sequence.
ACCESSION   AZ403083
VERSION   AZ403083.1   GI:10518157
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
             ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000   Std Error: 0.00
             Plate: 0170 row: P column: 09
             Seq primer: CACACAGGAAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 28.
FEATURES   Location/Qualifiers
     source   1..28
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0170P09"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|14732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

BASE COUNT   0 a   0 c   16 g   12 t

ORIGIN
        Query Match   0.4%;   Score 17; DB 17; Length 28;
        Best Local Similarity 100.0%; Pred. No. 1e+04;
        Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1147 AACCACCACCACCACCA 1163
             |||||||||||||||||
Db   24 AACCACCACCACCACCA 8

RESULT 8
H28644/c
LOCUS   H28644   40 bp   mRNA   linear   EST 13-JUL-1995
DEFINITION yl52h05.r1 Soares breast 3NDhBst Homo sapiens cDNA clone
            IMAGE:161913 5' similar to SP:A47476 A47476 MCl1 GENE PRODUCT=BCL2
            PRODUCT HOMOLOG - ;, mRNA sequence.
ACCESSION   H28644
VERSION   H28644.1 GI:898997
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 40)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 953
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality.
            Possible reversed clone: similarity on wrong strand
            Insert Length: 953   Std Error: 0.00
            Seq primer: M13Rev
            High quality sequence stop: 1.
FEATURES   Location/Qualifiers
     source   1..40
                     /organism="Homo sapiens"
                     /db_xref="GDB:57611;3"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:161913"
                     /clone_lib="Soares breast 3NDhBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCGCCCCCCCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     20. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT   7 a   10 c   5 g   15 t   3 others
ORIGIN
        Query Match   0.4%;   Score 17; DB 14; Length 40;
        Best Local Similarity 100.0%; Pred. No. 9.9e+03;

                      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   772 AAAAACGAAGAACGAATGT 788
             |||||||||||||||||||
Db   40 AAAAACGAAGAACGAATGT 24

RESULT 9
AZ637149/c
LOCUS   AZ637149   43 bp   DNA   linear   GSS 13-DEC-2000
DEFINITION 1M0496F19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0496F19 F, DNA sequence.
ACCESSION   AZ637149
VERSION   AZ637149.1 GI:11759339
KEYWORDS   GSS.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 43)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hanil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Weiss,D., Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0496   row: F column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 43.
FEATURES   Location/Qualifiers
     source   1..43
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0496F19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|, a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT   7 a   2 c   12 g   22 t
ORIGIN
        Query Match   0.4%;   Score 17; DB 17; Length 43;
        Best Local Similarity 100.0%; Pred. No. 9.8e+03;

RESULT 10

AZ315293/c

```
Qy    1152 CCACCACCACCAAAAACC 1168
           |||||||||||||||||||
Db      43 CCACCACCACCAAAAACC 27
```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
LOCUS       AZ315293               19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  IM0032P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0032P20 F, DNA sequence.
ACCESSION   AZ315293
VERSION     AZ315293.1  GI:10362003
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000    Std Error: 0.00
            Plate: 0032  row: P  column: 20
            Seq primer: CGTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0032P20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from the
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a       0 c      12 g       7 t
ORIGIN
```

Query Match   0.4%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;

RESULT 11

AZ622226/c

```
Qy    1148 ACCACCACCACCACCA 1163
           ||||||||||||||||
Db      18 ACCACCACCACCACCA 3
```

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
LOCUS       AZ622226               20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  IM0455A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0455A24 R, DNA sequence.
ACCESSION   AZ622226
VERSION     AZ622226.1  GI:11744416
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000    Std Error: 0.00
            Plate: 0455  row: A  column: 24
            Seq primer: CACCAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0455A24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a       0 c      14 g       6 t
ORIGIN
```

Query Match   0.4%; Score 16; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;

RESULT 12

Qy   1148 ACCACCACCACCACA 1163
           ||||||||||||||||
Db   18 ACCACCACCACCACA 3

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS   AZ784648/c
DEFINITION 2M0027P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0027P11 R, DNA sequence.
ACCESSION   AZ784648
VERSION   AZ784648.1 GI:12920600
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0027   row: P   column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES   Location/Qualifiers
     source   1..23
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0027P11"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT   2 a   5 c   7 g   9 t
ORIGIN

Query Match   0.48; Score 16; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;

RESULT 13

Qy   3409 ATCCAGTGGAAACAAG 3424
           ||||||||||||||||
Db   21 ATCCAGTGGAAACAAG 6

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS   AZ860972/c
DEFINITION 2M0167A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0167A16 F, DNA sequence.
ACCESSION   AZ860972
VERSION   AZ860972.1 GI:13056826
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0167   row: A   column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES   Location/Qualifiers
     source   1..23
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0167A16"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT   0 a   0 c   15 g   8 t
ORIGIN

Query Match   0.48; Score 16; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;

RESULT 14

Qy   1148 ACCACCACCACCACCA 1163
                ||||||||||||||||
Db   21 ACCACCACCACCACCA 6

Matches   16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

LOCUS   AZ449706   24 bp   DNA   linear   GSS 04-OCT-2000
DEFINITION   1M0248M02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0248M02 F, DNA sequence.
ACCESSION   AZ449706
VERSION   AZ449706.1   GI:10603768
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
             ,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000   Std Error: 0.00
             Plate: 0248   row: M   column: 02
             Seq primer: CGTTGTAAAACGACGGCCAGT
             Class: plasmid ends
             High quality sequence stop: 24.
FEATURES   Location/Qualifiers
     source   1..24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0248M02F"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptored DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|14732114|gb|AF129072.1|), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptored mouse DNA was annealed to
             adaptored vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
BASE COUNT   7 a   15 c   1 g   1 t
ORIGIN

Query Match   0.4%;   Score 16;   DB 17;   Length 24;
Best Local Similarity   100.0%;   Pred. No. 3.3e+04;

RESULT 15

Qy   1148 ACCACCACCACCACCA 1163
                ||||||||||||||||
Db   5 ACCACCACCACCACCA 20

Matches   16;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

LOCUS   AZ405428   26 bp   DNA   linear   GSS 03-OCT-2000
DEFINITION   1M0174D13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0174D13 F, DNA sequence.
ACCESSION   AZ405428
VERSION   AZ405428.1   GI:10529441
KEYWORDS   GSS.
SOURCE   house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
             ,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000   Std Error: 0.00
             Plate: 0174   row: D   column: 13
             Seq primer: CGTTGTAAAACGACGGCCAGT
             Class: plasmid ends
             High quality sequence stop: 26.
FEATURES   Location/Qualifiers
     source   1..26
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0174D13"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptored DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|14732114|gb|AF129072.1|), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptored mouse DNA was annealed to
             adaptored vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
BASE COUNT   0 a   0 c   17 g   9 t
ORIGIN

Query Match   0.4%;   Score 16;   DB 17;   Length 26;
Best Local Similarity   100.0%;   Pred. No. 3.3e+04;

Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1148 ACCACCACCACCACCA 1163
           |||||||||||||||||
Db   22 ACCACCACCACCACCA 7

Search completed: March 14, 2003, 08:29:38
Job time : 3697.82 secs